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Sequence 1, Appli
Sequence 2, Appli
Sequence 32356, A
Sequence 47573, A
Sequence 10729, A
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Sequence 2, A
Sequence 5999
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Sequence 28, Sequence 29,
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US-09-208-716-4
US-08-404-531B-9
                                                                                                                     -09-171-337A-6
           \begin{matrix} \mathbf{v} \\ \mathbf{v} 
               Sequence 39421, A
Sequence 54638, A
Sequence 11017, A
Sequence 3657, Ap
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                                                                                                                                                                                                                                                                          May 13, 2006, 08:14:12; Search time 46 Seconds (without alignments) 25.162 Million cell updates/sec
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                                                  GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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. /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
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. /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
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US-08-778-570B-12
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US-09-059-584-11
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Post-processing:

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Title: Perfect score:

Sequence:

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Scoring table:

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US-08-778-570B-12
US-08-778-570B-12
Sequence 12, Application US/08778570B
Sequence 12, Application US/08778570B
SEDERAL INFORMATION:
APPLICANT: GALTYVERS, Anthomy B
APPLICANT: Loosmore, Sheena M.
APPLICANT: Harkness, Robin E
APPLICANT: Yang, Yan-Ping
APPLICANT: Yan-Ping
APPLICANT: Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yan-P
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schryvers, Anthony B
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Hosmore, Sheena M.
APPLICANT: Van-Ping
APPLICANT: Van-Ping
APPLICANT: Klein, Michel H
ITIME OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Gth Floor, 330 University Avenue
CITY: Touronto
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COUNTRY: Canada
ZIP: WGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RALES
CURRENT APPLICATION DATA:
FILING DATE: PATENTIN RALES
FILING DATE: STEMAR-1996
CLASSIFICATION: 435
FILING DATE: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-542
TELEPHONE: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-542
TELEPHONE: (416, 595-1165)
TELEPHONE: (416, 595-1165)
TELEPHONE: (416, 595-1163)
INFORMATION POR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
US-08-613-009A-10
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100.0%; Score 74; DB 2; Seat Local Similarity 100.0%; Pred. No. 1.9e-05; Matches 14; Conservative 0; Mismatches 0;
ALIGNMENTS
                                                                                                                                                                                                                  Sequence 10, Application US/08613009A
Patent No. 6090576
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APPLICANT: Du, Kun-Pan
APPLICANT: Wang, Van-Pan
APPLICANT: Wang, Van-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OP SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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100.0%; Score 74; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: Sim & McBurey
STREET: 6th Floor, 330 University Avenue
CITY: Toxonto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-UN-1997
CLASSIFICATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-681 MIS:jb
TELECOMMUTCATION INFORMATION:
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TELEFACOMMUTCATION OF SSE-1155
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TELEFACOMMUTCATION: 25:
SEQUENCE CHARACTERISTICS:
                                                                              1038-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038
TELECHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TYPE: amino acid
US-09-059-584-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 MGYGMALSKINLHN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGYGMALSKINLHN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-867-941-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-867-941-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Patent No. 6184371

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Run-Pan Du
APPLICANT: Yang, Yan-Ping
APPLICANT: Xien, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
INVHER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                         APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Hosenore, Sheena M.
APPLICANT: Losenore, Sheena M.
APPLICANT: Ju, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 74; DB 2; Length 702; 100.0%; Pred. No. 2e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Uncaration
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,009A
FILING DATE: 08-MAR.1996
CLASSIFICATION NUMBER: 1936
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-542
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER.STICS:
LENGTH: 702 amino acide
TYPE: amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
            Sequence 9, Application US/08613009A Patent No. 6090576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 MGYGMALSKINLHN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGYGMALSKINLHN 14
                                         Patent No. 6090576
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.1
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
TOPOLOGY:
US-08-613-009A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-074-658-25
US-08-613-009A-9
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GENERAL INFORMATION:
APPLICANT: Wyers, Lisa E
APPLICANT: Schryers, Anthony B
APPLICANT: Schryers, Robin E
APPLICANT: Locsmore, Sheena M.
APPLICANT: Locsmore, Sheena M.
APPLICANT: Locsmore, Sheena M.
APPLICANT: Asnay, Yan-Pan
APPLICANT: Klein, Michel H
ITILE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STREET: Gth Floor, 330 University Avenue
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 74; DB 2; Length 702;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada

COUNTRY: Canada

ZIP, MGG IR7

COMPUTER READABLE FORM:
MGDIUM TYPE: Floppy disk
COMPUTER: CANADALLA

COMPUTER: CANADAL

COMPUTER: CANADAL

COMPUTER: CANADAL

COMPUTER: CANADAL

CANADAL

CANADAL

RELIAND NUMBER: US 08/778,570

FILING DATE: 03-JAN-1997

CLASSIFTCATION:

APPLICATION NUMBER: US 08/778,570

FILING DATE: 03-JAN-1997

CLASSIFTCATION

ATTONEWY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24973

TELECHONE: (416) 595-1155

TELECHONE: (416) 595-1155

TELECHONE: (416) 595-1155

TELECHONE: (416) 595-1155

TELECHONE: CANADATERSTICS:

LEWINDORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERSTICS:

LEWINDORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-059-584-11
; Sequence 11, Application US/09059584
; Patent No. 6440701
                    ; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-778-570B-11
                                                                                                                                                                                                                                                                                                                                                                                                 100 MGYGMALSKINLHN 113
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPCLGY: linear
US-09-059-584-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGYGMALSKINLHN 14
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Sequence 11, Application US/08778570B

Patent No. 6437096

GENERAL INFORMATION:

APPLICANT: Schryvers, Anthony B

APPLICANT: Schryvers, Anthony B

APPLICANT: Barress, Renem M.

APPLICANT: Loosence, Sheena M.

APPLICANT: Yang, Yan-Ping

APPLICANT: Yang, Yan-Ping

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H

ITITE OF INVENTION: Transferrin Receptor Genes of Moraxella

NUMBER OF SEQUENCES. 43

COMPRESSEE: Sim & McBurney

STREET: Gir Floor, 330 University Avenue

COUNTRY: Canada

ZITE MGG IR7

COUNTRY: Canada

ZITE MGG IR7

COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Batenin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: 24973

APPLICATION NUMBER: 24973

REGISTRATION NUMBER: 24973

REGISTRATION NUMBER: 24973

REGERRANCE/DOCKET NUMBER: 1038-664

TELEPHONE: (416) 595-1155
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUCTWARE: Petentin Release #1.0, Version #1.30
STING DATE: 08-MAY-1988
FILING DATE: 08-MAY-1988
FILING DATE: 08-MAY-1988
FILING DATE: 08-MAY-1988
ILLASSIFICATION: 435
ATYORNEY/AGENT INFORMATION:
NAME: Stewart, Michael II
NAME: Stewart, Michael II
NAME: Stewart, Michael II
NAME: STEWART/ONCKET NUMBER: 24,973
FELERENCE/DOCKET NUMBER: 1038-795
FELERENCE/COCKET NUMBER: 1155
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LEMETH: 702 and 10 acids
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LEMETH: 702 and 10 acids
STEANUBEDNESS: single
STEANUBEDNESS: single
JUS-09-074-658-25
INOO.08; SCOIF 74; DB 2; L/
DE-001-08; SCOIF 74; DB 2; L/
DE-001-08-08-08; DE-005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 MGYGMALSKINLHN 113
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Sequence 91, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Daniel
Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                        ADDAL
STREET: 01...
TTTY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-907-794A-91
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APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
                                                                                                                                                                                                                                               APPLICANT: Myers, Lisa E
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCES: 60
CORRESPONDENCES: 61
ADDRESSES: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 2; Length 706;
Pred. No. 0.00097;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REGISTRATION NUMBER: 24973
REGISTRATION NUMBER: 24973
REJERPANCE/DOCKET NUMBER: 1038-794
TELEPHONE: (416) 595-1165
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6th Floor, 330 University
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49, Application US/09059584
Patent No. 6440701
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Losemore, Sheena M.
APPLICANT: Do, Run-Pan
                                                                                                                                                       Sequence 46, Application US/09059584 Patent No. 6440701 GENERAL INFORMATION:
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100 MGYGMALSKINLHN 113
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Best Local Similarity 92.3
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                                                                                               RESULT 9
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Pred, No. 0.0023;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,584

FILING DATE: 14-APR-1998

CLASSIFICATION 14-APR-1998

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/778,570

FILING DATE: 03-JAN-1997

CLASSIFICATION NUMBER: 103-794

APPLICATION NUMBER: 24973

REGISTRATION NUMBER: 24973

REGISTRATION NUMBER: 1038-794

TELECOMMULCATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFRAK: (416) 595-1165

TELEFRAK: CHANG SEQ ID NO: 49:

SEQUENCE CHARACTER STICS:
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Meburney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.1%;
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Best Local Similarity 85.7
Matches 12; Conservative
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APPLICANT: STEWART, 11MOCHY A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION WHORE: US/09/905,125A
CURRENT APPLICATION NUMBER: US/00/04414
PRIOR APPLICATION NUMBER: BCT/US0/04414
PRIOR FILING DATE: 1990-07-07
PRIOR PLING DATE: 1990-07-07
PRIOR PLING DATE: 1990-07-07
PRIOR PLING DATE: 1990-07-08
PRIOR PLING DATE: 1990-07-08
PRIOR PLING DATE: 1990-09-08
PRIOR PLING DATE: 1990-09-01
PRIOR PLING DATE: 1990-01-13
PRIOR PLING DATE: 1990-01-13
PRIOR PLING DATE: 1990-10-13
PRIOR APPLICATION NUMBER: PCT/US99/2056
PRIOR APPLICATION NUMBER: PCT/US99/2056
PRIOR APPLICATION NUMBER: PCT/US99/3009
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30099
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Pred. No. 20;
4; Mismatches 0; Indels
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Paoni, Nicholas F.
Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 63.6
Matches 7; Conservative
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US-09-905-125A-91
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US-09-902-775A-91
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INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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Pred. No. 20;
4; Mismatches 0; Indels
                          TITLE OF INVENTION: Secreted and Transmembrant TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/907,794A CURRENT FILING DATE: 2001-02-22 PRIOR PELICATION NUMBER: US 60/145,698 PRIOR PELING DATE: 1995-07-07 PRIOR PELING DATE: 1995-07-07 PRIOR PELING DATE: 1995-07-26 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR APPLICATION NUMBER: PCT/US99/20594 PRIOR PELING DATE: 1995-09-08 PRIOR PELING DATE: 1995-09-18 PRIOR PELING DATE: 1995-09-18 PRIOR PELING DATE: 1995-09-18 PRIOR PELING DATE: 1995-09-15 PRIOR PELING DATE: 1995-10-05 PRIOR PELING DATE: 1995-10-05 PRIOR PELING DATE: 1995-10-05 PRIOR PELING DATE: 1995-11-20 PRIOR APPLICATION NUMBER: PCT/US99/20313 PRIOR PELING DATE: 1995-11-20 PRIOR APPLICATION NUMBER: PCT/US99/20301 PRIOR PELING DATE: 1995-11-20 PRIOR APPLICATION NUMBER: PCT/US99/20301 PRIOR PELING DATE: 1995-11-20 PRIOR APPLICATION NUMBER: PCT/US99/20301 PRIOR PELING DATE: 1995-11-20 PRIOR PELING DATE: 1995-12-06 PRIOR PELING DATE: 1995-12-07 PRIOR PELING DATE: 2995-12-07 PRIOR PEUTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 91, Application US/09905125A; Patent No. 6664376; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Generacch, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Buterein, David
APPLICANT: Betterin, David
APPLICANT: Betterin, David
APPLICANT: Esten, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Giang
APPLICANT: Gerier, Hanspeter
APPLICANT: Gerier, Mary E.
APPLICANT: Gerier, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%;
illarity 63.6%;
Conservative 4
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; ORGANISM: Homo sapiens
US-09-907-794A-91
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Best Local Similarity
Matches 7; Conserva
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US-09-905-125A-91
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10

PRIOR PRICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-38

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR PRILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR PRILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-10-03

PRIOR PRILING DATE: 1999-10-03

PRIOR PRILING DATE: 1999-10-03

PRIOR P
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, P. Mickey
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P.
      Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: Homo sapiens
US-09-902-775A-91
                                                                                                                                                                                                                                                                                                                                                                         Goddard, A.
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APPLICANT:
APPLICANT:
             APPLICANT:
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Score 42; DB 2; Length 696; Pred. No. 20;

56.8%;

Query Match Best Local Similarity

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APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT PELING DATE: 1046-700
CURRENT PILING DATE: 1046-700
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-36
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR PELING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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                                                                                                                                                                                                      Sequence 91, Application US/09906700
Patent No. 6723535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Genertech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                        493 GVSLSKLSLHN 503
4 GMALSKINLHN 14
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                                                                                                                                                      RESULT 14
JS-09-906-700-91
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APPLICANT:
APPLICANT:
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Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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CRGANISM: Homo sapiens
US-09-903-603A-91
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APPLICANY: Forgy, Sherman
APPLICANY: Gao, Wei-Giang
APPLICANY: Gao, Wei-Giang
APPLICANY: Gactber, Hanspeter
APPLICANY: Gerber, Hanspeter
APPLICANY: Gerther, May B. J.
APPLICANY: Goddard, A. J.
APPLICANY: Grimaldi, Christopher J.
APPLICANY: Gianaldi, Christopher J.
APPLICANY: Marber, Jennie D.
APPLICANY: Mather, Jennie D.
APPLICANY: Walliam, Kenneth, J.
APPLICANY: Walliam, Wicholas F.
APPLICANY: Walliams, Daniel
APPLICANY: Paoni, Nicholas F.
APPLICANY: Walliams, P. Mickey
BRIOR FILING DATE: 1999-07-26
PRIOR APPLICANY: WAMBER: PCT/US99/2109
PRIOR APPLICANY: WAMBER: PCT/US99/2109
PRIOR APPLICANY: WAMBER: PCT/US99/2109
PRIOR APPLICANY: WAMBER: PCT/US99/2109
PRIOR APPLICANTION WAMBER: PCT/US99/2167
PRIOR APPLICANTION WAMBER: PCT/US99/2109
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Pred. No. 20;
4; Mismatches 0; Indels
| PRIOR FILING DATE: 1999-12-20
| PRIOR APPLICATION NUMBER: PCT/US00/00219
| PRIOR FILING DATE: 2000-01-05
| NUMBER OF SEQ ID NOS: 423
| SEQ ID NO 91
| LENGTH: 696
| TYPE: PRT
| ORGANISM: HOMO SapienS
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PRIOR PEPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-903-603A-91
; Sequence 91, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Best Local Similarity 63.6%;
Matches 7; Conservative
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APPLICANT: Goddward, Paul J.
APPLICANT: Goddward, A.
APPLICANT: Goddward, A.
APPLICANT: Grimald; Christopher J.
APPLICANT: Hillan, Kameth, J.
APPLICANT: Hillan, Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Maillams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FITLE OF INVENTION: Secreted and Transmembrane Polypeptides
FILE OF INVENTION: Secreted
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT APPLICATION NUMBER: US/09/04114
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
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Pred. No. 20;
4; Mismatches 0; Indels
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION WUMBER: PCT/US99/28564
PRIOR APPLICATION WUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR PRILOR DATE: 1999-12-16
PRIOR APPLICATION WUMBER: PCT/US99/30991
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION WUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION WUMBER: PCT/US99/30999
PRIOR APPLICATION WUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 91
LEAGHING DATE: 2000-01-05
SEQ ID NO 91
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US-09-904-920A-91
; Sequence 91, Application US/09904920A
; Patent No. 68065152
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.;
; APPLICANT: Genentech, Inc.;
; APPLICANT: Botstein, David
; APPLICANT: Benenyers, Luc
; APPLICANT: Benenyers, Luc
; APPLICANT: Fatron, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Forg, Sherman
; APPLICANT: Geney, Relen
; APPLICANT: Geney, Hanspeter
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geney, Mary E.
; APPLICANT: Geney, Mary E.
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TITLE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT PILIOR DATE: 2001-07-18

RIOR APPLICATION NUMBER: US/09/909,064

CURRENT PILIOR DATE: 2001-07-18

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03

PRIOR PILI
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Sequence 91, Application US/09905381A
Patent No. 6818746
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Gao, Wei-Qiang
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493 GVSLSKLSLHN 503
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ORGANISM: Homo sapiens
US-09-909-064-91
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Best Local Similarity
Matches 7; Conserv
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APPLICANT:
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APPLICANT:
APPLICANT:
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Pred. No. 20;
4; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PRILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
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US-09-90-64-91
US-09-909-64-91
Sequence 91, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.,
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baten, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Foly, Sherman
APPLICANT: Foly, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Goddwski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Roy, Margaret Ann
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Gerritsen, Mary E.
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Stewart, ....
Daniel
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493 GVSLSKLSLHN 503
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CRGANISM: Homo sapiens
US-09-904-920A-91
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APPLICANT:
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INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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Pred. No. 20;
4; Mismatches 0; Indels
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
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Pred. No. 20;
4; Mismatches 0; Indels
Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative 6

RESULT 19
US-09-06-618-91
Sequence 91, Application US/09906618
Fatent No. 6828146
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR PELICATION NUMBER: PTT/USO/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: WS 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/2164
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/904,462

CURRENT FILING DATE: 2000.07.13

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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493 GVSLSKLSLHN 503
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                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-646-91
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Matches 7; Conserv
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APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERDER. 10466-14
CURRENT APPLICATION WHERE: US/09/906,646
CURRENT FILING DATE: 2002-01-22
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PRIOR PLING DATE: 2002-01-22
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-28
PRIOR PLLING DATE: 1999-09-18
PRIOR PLLING DATE: 1999-09-18
PRIOR PLLING DATE: 1999-09-13
PRIOR PLLING DATE: 1999-09-13
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-10-05
PRIOR PLLING DATE: 1999-10-05
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                      Sequence 91, Application US/09906646 Patent No. 6852848 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E
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Paoni, Nicholas F.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei-Qiang
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493 GVSLSKLSLHN 503
4 GMALSKINLHN 14
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Gaps
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                                                                                                                                     Length 696;
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                                                                                                                                     Score 42; DB 2;
Pred. No. 20;
4; Mismatches
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 91
LENGTH: 696
                                                                                                                                                                                                                                                                                                Sequence 91, Application US/09904462
Patent No. 6878807
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
                                                                                                                                      56.8%;
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Gerritsen, Mary E
                                                                                                                                                                     Conservative
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Gao, Wei-Qiang
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Tumas, Daniel
Williams, P. Mickey
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Best Local Similarity 63.6%;
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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CAGANISM: Homo sapiens
US-09-902-736A-91
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: 05/99/902,736A
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2; Length 696;
Pred. No. 20;
4; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kilavin, Ivar J.
Mather, Jennie P.
Pan, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Sequence 91, Application US/09902736A
Patent No. 6894148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 GVSLSKLSLHN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GMALSKINLHN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                  type: PRT CORGANISM: Homo Sapien US-09-904-462-91
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Gaps
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Pred. No. 20;
4; Mismatches 0; Indels
HENCR FLIAGO LATE: 1999-10-28

PRICOR PLICAGO LATE: 1999-09-08

PRICOR PLING DATE: 1999-09-08

PRICOR PLING DATE: 1999-09-08

PRICOR PLING DATE: 1999-09-18

PRICOR PLING DATE: 1999-09-15

PRICOR PLING DATE: 1999-10-05

PRICOR PLING DATE: 1999-10-05

PRICOR PLING DATE: 1999-11-29

PRICOR PLING DATE: 1999-11-29

PRICOR PLING DATE: 1999-11-20

PRICOR PLING DATE: 1999-12-02

PRICOR PLING DATE: 1999-12-03

PRICOR PLING DATE: 1990-12-03

PRICOR PLING DATE: 2000-01-05

PRICOR PLING DATE: 2000-01-05
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US-09-906-722A-91
; Sequence 91, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Genentech, David
nopt,ICANT: Bocstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddwrki, Paul J.
Gurmey, Austin L.
Hillan, Kenneth, J.
Kilavin, Ivar J.
Mather, Jennie P.
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Gaps

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Length 81; Indels

DB 2; 4.1;

Score 40; DB 2 Pred. No. 4.1; 3; Mismatches

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OTHER INFORMATION: Xaa means any amino acid
                                                                                          54.1%;
53.8%;
                                                                                                                                                                                                            2 GYGMALSKINLHN 14
                                                                                                                                                                                                                                             45 GYMHSIPRINLHN 57
                                                                                             Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                 US-09-270-767-39421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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APPLICANT: Wood, william, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1618-201-07-16
CURRENT PILLING DATE: 2001-07-16
FRIOR PLICATION NUMBER: US/09/906,722A
CURRENT FILLING DATE: 2000-07-16
FRIOR PLICATION NUMBER: US/09/906,722A
FRIOR PLICATION NUMBER: 195-07-07
FRIOR PLICATION NUMBER: US 60/143,048
FRIOR PLICATION NUMBER: US 60/143,048
FRIOR PLICATION NUMBER: PCT/US99/2054
FRIOR PLICATION NUMBER: PCT/US99/2054
FRIOR PLICATION NUMBER: PCT/US99/2054
FRIOR PLICATION NUMBER: PCT/US99/2054
FRIOR PLICATION NUMBER: PCT/US99/2050
FRIOR PLICATION NUMBER: PCT/US99/30095
FRIOR PLICATION NUMBER: PCT/US99/30095
FRIOR PLICATION NUMBER: PCT/US99/30095
FRIOR PLICATION NUMBER: PCT/US99/30095
FRIOR PLICATION NUMBER: PCT/US99/30099
FRIOR PRICING DATE: 1999-12-02
FRIOR PRICING DATE: 1999-12-02
FRIOR PRICING DATE: 1999-12-02
FRIOR PRICING NUMBER: PCT/US99/30099
FRIOR PRICING DATE: 1999-12-05
FRIOR PRICING DATE: 2000-01-05
FRIENDER: PRICING DATE: 2000-01-05
FRIENDER: PRICING DATE: 2000-01-05
FRIENDER: PRICING DATE: 2000-01-05
FRIENDER:
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Batent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39421
LENGTH: 81
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-906-722A-91
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Best Local Similarity
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US-09-270-767-39421
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RESULT 26
US-09-902-540-11017

i Sequence 11017, Application US/09902540

j Patent No. 6833447

general INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Greeory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
CURRENT APPLICATION UNMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 11017
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                                                                              GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Serence: 7326-094
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54638
LENGTH: 81
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Pred. No. 42;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%; Score 40; DB; 53.8%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                            ; CTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
RESULT 25
209-270-767-54638
; Sequence 54638, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53...
Tri Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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Gaps
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RODRIGHEZ SALZ, Marte
COLLADOS DE LA VIELA, Alfonso J.
MORENO VALLE, Migeul Angel
SALTO MALDONALOC, Francisco
DIEZ CARCIA, BRUNOZERS OF THE GENES GLUTAMATE
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGERASE, AND -ACTIVILEXORAMINIDASE
AND -ACTIVI AND THEIR USE IN FILLAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 41;
4; Mismatches 3; Indels
                                                                                                       Score 38; DB 2; Length 282;
Pred. No. 41;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09221014C
Sequence 32, Application US/09221014C
Sequence 32, Application US/09221014C
SEMERAL INFORMATION:
APPLICANT: Rosson, Reinhardt D.
APPLICANT: Grund, Alan D.
APPLICANT: Sanchez-Riera, Fernando
ITILE OF INVENTION: LINOLEATE ISOMERASE
ITILE DOF INVENTION: LINOLEATE ISOMERASE
FILE REFERENCE: 3161-20
CURRENT FILING DATE: 1997-12-23
CURRENT FILING DATE: 1997-12-23
EARLIER PETLING DATE: 1997-12-23
EARLIER FILING DATE: 1997-12-23
EARLIER FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 32
LENGTH: 282
LENGTH: 282
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09171337A Patent No. 6300095
GENERAL INFORMATION:
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-561-0770-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Lactobacillus reuteri
US-09-221-014-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.4%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                               Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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132 LNYGIWLNKVRLH 144
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US-09-171-337A-6
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US-09-221-014-32
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             Sequence 3657, Application US/09134000C

Fatent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Douette-Stamm et al
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUCLES: US/09/134,000C
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOGTWARE: Patentin Version 3.1
SEQ ID NO 3657
LENGTH: 315
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Best Local Similarity 50.0%; Pred. No. 17;
Matches 6; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 2; Length 315;
Pred. No. 30;
4; Mismatches 1; Indels
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Patent No. 6706501

GREAL INFORMATION:
APPLICAWT: Rosson, Reinhardt D.
APPLICAWT: Bosson, Richard D.
APPLICAWT: Grund, Alan D.
TITLE REPERENCE: JAG-20-C1
CURRENT APPLICATION NUMBER: US/09/561,077C
CURRENT PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/141,798
PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7870
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3657
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Similarity 54.5%;
6; Conservative
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99 WGMAMSAISIHS 110
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25 GFGLAITKFNL 35
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Best Local Similarity
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US-09-328-352-7870
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Matches
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0; Mismatches
                   APPLICATION NUMBER: US/09/631,022
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Penicillum chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetylhexosaminidase enzyme (EC.3.2.1.52) with a a molecular weight of 66545 Da. SEQUENCE DESCRIPTION: SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                        TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/09830807; Patent No. 6846667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S0.7%;
Best Local Similarity 81.8%;
Matches 9; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-830-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 62.5
Matches 10; Conservative
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US-09-830-807-7
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-MAY-1999
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-WAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-WAR-1997
ATTORNEY/ADENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WOOTDERfect 8 for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Penicillum chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetylhexosaminidase enzyme (EC.3.2.1.52) with a molecular weight of 6545 Da. SEQUENCE DESCRIPTION: SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: LADAS & PARRY
STRRET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09631022
Patent No. 6558921
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.7
Best Local Similarity 81.8
Matches 9; Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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US-09-631-022-6
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APPLICANT: Clarke, Enda E.

APPLICANT: Clarke, Enda E.

APPLICANT: Clarke, Enda E.

APPLICANT: Clarke, Enda E.

APPLICANT: Bererest, Paul H.

APPLICANT: Bougan, Gordon

APPLICANT: Bougan, Robert G.

APPLICANT: Feldman, Robert G.

TITLE OF INVENTION: VIRULENCE GENES AND PROTEINS, AND THEIR USE

FILE REFERENCE: GJE.

CURRENT APPLICATION NUMBER: US/09/830,807

CURRENT FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 72

SEQ ID NOS: 72

SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.5; DB 2; Length 596;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels 1
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FILING DATE: 02-Aug-2000
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: B00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
(C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 37; DB 2; 62.5%; Pred. No. 7.2;
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; LENGTH: 228
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9719
                                  ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6509
                                                                                                                                                                                                                                                                                                              US-09-949-016-9719
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Sequence 6509, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-09
PRIOR FILING DATE: 2000-0-09
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                             J. Sequence 3734, Application US/09270767

J. Sequence 3734, Application US/09270767

J. Patent No. 6703491

J. Patent No. 6703491

J. PITLE NORMATION: Modelec et al.

J. TITLE OF INVENTION: Modelec acids and proteins of Drosophila melanogaster.

J. TITLE PORTERIOR: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 37334

LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 2; Length 167; Pred. No. 35; 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 37; DB 2; Length 167; Best Local Similarity 61.5%; Pred. No. 35; Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52551
                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37334
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 1
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RESULT 34
US-09-270-767-37334
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NESULT 38
US-09-134-000C-6538
US-09-134-000C-6538

Sequence 6538, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BUTERCCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION WUMBER: US/09/134,000C
CURRENT PAPLICATION WUMBER: US 60/055,778
PRIOR APPLICATION WUMBER: US 60/055,778
PRIOR PILING DATE: 1999-08-15
NUMBER OF SEQ ID NOS: 6812
SOUTHARE: Betentin version 3.1
SEQ ID NO 6538
LENGTH: £18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

SOFTWARE: FREEER 2000-09-08

SOFTWARE: FREEER 2000-09-08

SOFTWARE: PREEER FREEER FRE
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                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 37; DB 2; 50.0%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6509
LENGTH: 217
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US-09-134-000C-6538
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Best Local Similarity 50...
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Best Local Similarity 50.0
Matches 6; Conservative
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Sequence 724, Application US/09949016

Sequence 724, Application US/09949016

Sequence 724, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FRICK REPERRENT SOUGH 307

CURRENT APPLICATION NUMBER: 60/231, 768
PRIOR PLILNG DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLILNG DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7724
                                                                                                                                                                                                                                                           Sequence 6344, Application US/09949016
; Sequence 6344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICAMTY VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REPERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PELLING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6354
; LENGTH: 351
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49.3%; Score 36.5; DB 2; Length 357;
Best Local Similarity 31.0%; Pred. No. 1e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 18
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49.3%; Score 36.5; DB 2; Length 351;
Best Local Similarity 31.0%; Pred. No. 1e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 15
Best Local Similarity 53.8%; Pred. No. 1.5e+02; Matches 7; Conservative 1; Mismatches 5; Indels
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136 VGFGEAISKQFVDALETGQDARAAMNLHN 164
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                                                                                        2 GYGMALSKINLHN 14
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; ORGANISM: Human
US-09-949-016-6354
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US-09-949-016-6354
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142 VGFGEAISKQFVDALETGQDARAAMNLHN 170
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Search completed: May 13, 2006, 08:15:31 Job time : 48 secs

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25 42 56.8 696 6 ABU66746 26 42 56.8 696 6 ABU54362 27 42 56.8 696 6 ABU54377 28 42 56.8 696 6 ABU59827 29 42 56.8 696 6 ABU59817 30 42 56.8 696 6 ABU54514	42 56.8 696 6 42 56.8 696 6 42 56.8 696 6 56.8 696 6	42 56.8 696 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	42 56.8 696 6 42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6 42 56.8 696 6 40 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6	42 56.8 696 6 42 56.8 696 6	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7	42 56.8 696 7
version 5.1.8 - 2006 Biocceleration Ltd.	Search time 185 Seconds (without alignments) 33.250 Million cell updates/sec			residues	parameters: 2443163		ries						predicted by chance to have a	score of the result be otal score distribution	ARIES	-	Descript		Adv70479	Aaw35313 Aav43383	Aay43378	Aaw35316 Abm69725	Adi36920	Aay94963 Aay08076	Aay13359	Adc78411	Aab80227	Adu00824 Adu12348	Aab50905	Abu71605 Abo17792	Abu71460	Abu81046 Abu71906	Aboul789 Novel hu
GenCore ver Copyright (c) 1993 - 2 OM protein - protein search, using sw mo	Run on: May 13, 2006, 08:06:48 ;	Title: US-10-769-514-17 Perfect score: 74 Sequence: 1 MGYGMALSKINLHN 14	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2443163 segs, 439378781	tisfying chosen	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summarie	A_Geneseq_21:*	geneseqp2008 geneseqp20008	geneseqp2001s:		geneseqp20048: geneseqp20058:	the number of	score greater than or equal to the and is derived by analysis of the t	SUMMARI	Query	Score Match Length DB	74 100.0 14 9	74 100.0 15 9	74 100.0 702 2	65 87.8 706 2	63 85.1 714 2 . 46 62.2 190 6	42 56.8 635 8	42 56.8 695 3 42 56.8 696 2	42 56.8 696 2	42 56.8 696 3 42 56.8 696 3	42 56.8 696 4	42 56.8 696 4 42 56.8 696 4	42 56.8 696 4	42 56.8 696 6 42 56.8 696 6	42 56.8 696 6	22 42 56.8 696 6 ABU81046 23 42 56.8 696 6 ABU71906	42 56.8 696 6

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WPI; 2005-038740/04.
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                                          US2004258695-A1.
                                                                                                                                                                                                                                                                                                Sequence 15 AA;
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                                                            23-DEC-2004
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bacterial transferrin binding proteins, which block bacterial transferrin
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                                                                                                                                                        bacterial infection; antibacterial; bacterial meningitis; antibacterial; neuroprotective; otitis media; auditory; transferrin binding protein B.
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                                                                                                                                        Moraxella catarrhalis transferrin binding protein B region - SEQ ID 17.
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Adb29007 Human Pl
Ada76959 Human Pl
Ada88589 Novel h
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                                            ALIGNMENTS
ADB29007
ADA76959
ADA88589
                                                                                                                                                                                                                                                                                                                                                             Claim 7; SEQ ID NO 17; 27pp; English.
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                                                                                     ADV70480 standard; peptide; 14 AA
                                                                                                                                                                                                                                      30-JAN-2004; 2004US-00769514.
                                                                                                                                                                                                                                                      31-JAN-2003; 2003US-044113P.
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969
                                                                                                                                                                                   Moraxella catarrhalis
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56.8
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56.8
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bacterial infection; antibacterial; bacterial meningitis; antibacterial;
neuroprotective; otitis media; auditory; transferrin binding protein B.
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                                                                                                                       Moraxella catarrhalis,
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                    Transferrin-binding molecules useful for eliciting antibodies to
bacterial transferrin binding proteins, which block bacterial transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding transferrin receptor of a Moraxella strain - also proteins, ful in vaccines, as diagnostic agents and in the production of
                                                                                                                                                                                                             The invention comprises a molecule (e.g. peptide) which is capable of: binding to a region of a transferrin protein that is recognized by a bacterial transferrin binding protein; and eliciting an antibody to the bacterial transferrin binding protein. The transferrin binding molecule of the invention is useful for preventing and treating bacterial infections (e.g. bacterial meningitis and otitis media). The present amino acid sequence represents a region of the Moraxella catarrhalis transferrin binding protein B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 74; DB 9; Length 15; 100.0%; Pred. No. 6.4e-07; Live 0; Mismatches 0; Indels
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                                                                                                                                                          Example 1; SEQ ID NO 16; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-CA000163.
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97US-00778570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGYGMALSKINLHN 14
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Best Local Similarity luv...
Local Similarity luv...
Local 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1996;
03-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998
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antibodies.
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Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW35313;
                                                                                                   uptake.
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AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding transferrin binding protein 2 of Moraxella catarrhalis, useful for diagnostics, immunization and recombinant protein
                                                                                                                                                                                                                                                                                                                                                       TbpB gene; Tbp2; transferrin binding protein; diagnosis; otitis media; genetic immunisation; Moraxella infection; antigen; vaccine; detection; antitumour antibody production; therapy.
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang Y;
e.g. for diagnosis or gene isolation, by usual hybridisation assays
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                                                             Length 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                             Indels
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100.0%; Pred. No. 5.2e-05;
iive 0; Mismatches 0;
                                                           ; Score 74; DB 2; I
; Pred. No. 5.2e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                M. catarrhalis strain 4223 tbp2 protein.
                                                                                                                                                                                                                                    AAY43383 standard; protein; 702 AA.
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                                                                  100.0%;
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                                                                                                                                                MGYGMALSKINLHN 113
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                                                                                                                            1 MGYGMALSKINLHN 14
                                                                                                                                                                                                                                                                                                 26-JAN-2000 (first entry)
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                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis
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                                                                              Best Local Similarity
Matches 14; Conserv
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                                   Sequence 702 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production.
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Klein MH;
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                                                                   Query Match
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Matches
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Local Similarity 85.7
les 12; Conservative
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                                        Moraxella catarrhalis.
                                                                                                                                                                                                             WPI; 1997-457533/42.
N-PSDB; AAT95251.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 714 AA;
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                                                                                                      07-MAR-1997;
                                                                                                                          08-MAR-1996;
03-JAN-1997;
                                                            WO9732980-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2002
                                                                                                                                                                                                                                                                  antibodies.
                                                                                                                                                                              Myers LE,
Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM69725;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the Moraxella catarrhalis strain M35 transferrin binding protein (TDp2) of the invention. The DNA sequence is also referred to as the TDpB gene. The TDpB sequence is also referred to as identification or diagnosis of Moraxella, or for cloning related species, using Mybridiation asaays; and for genefit immunisation against Moraxella infections, e.g. ottis media. The TDp2 proteins are useful as antigens, either in vaccines (including components of conjugate vaccines that contain antigens from other bacteria or from tumours, in which case they elicit production of antitumour antibodies that may be coupled to chemotherapeutic agents or biologically active agents) or to raise antibodies (for use as diagnostic reagents and for treating Moraxella infections), also for detecting Moraxella antibodies
                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding transferrin binding protein 2 of Moraxella catarrhalis, useful for diagnostics, immunization and recombinant protein production.
                                                                                                                          TopB gene; Top2; transferrin binding protein; diagnosis; otitis media; genetic immunisation; Moraxella infection; antigen; vaccine; detection; antitumour antibody production; therapy.
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                                                                                                                                                                                                                                                                                                  Yang Y;
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                                                                                                                                                                                                                                                                                                  Du R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 65; DB 2; Length 706; 92.3%; Pred. No. 0.0028; trive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 Myers LE, Schryvers AB, Harkness RE, Loosmore SM,
Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. catarrhalis R1 transferrin binding protein tbpB.
                                                                                                         M. catarrhalis strain M35 tbp2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW35316 standard; protein; 714 AA.
                                          AAY43378 standard; protein; 706 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 2; 114pp; English.
                                                                                                                                                                                                                                    99WO-CA000307.
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                                                                                    (first entry)
                                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD.
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es 12; Conservative
                                                                                                                                                                       Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-620376/53.
N-PSDB; AAZ31946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 706 AA;
                                                                                                                                                                                            WO9952947-A2.
                                                                                                                                                                                                                                    12-APR-1999;
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                                                                                    26-JAN-2000
                                                                                                                                                                                                                 21-OCT-1999
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                                                               AAY43378;
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Matches
                     RESULT 7
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The present sequence is the Moraxella catarrhalis R1 transferrin binding protein tbpB, which can be used as an immunogen, e.g. in vaccines to protect against diseases caused by M. catarrhalis (specifically otitis media), or to raise antibodies for diagnosis and therapy. It can also be used as a carrite for other antigens determinants, e.g. of bacteria containing polysaccharide antigens or abnormal polysaccharides present tumour cells, particularly to make conjugate vaccines. The tbpB DNA can be used to detect mucleic acid encoding transferrin receptor protein, e.g. for diagnosis or gene isolation, by usual hybridisation assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding transferrin receptor of a Moraxella strain - also proteins, useful in vaccines, as diagnostic agents and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Du R, Yang Y;
Transferrin binding protein; tbpB; immunogen; vaccine; protection; otitis media; antibody; diagnosis; therapy; carrier; gene isolation
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85.7%; Pred. No. 0.0067;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schryvers AB, Harkness RE, Loosmore SM,
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                                                                                                                                                                                                                                                                                                                                                          97WO-CA000163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00613009.
97US-00778570.
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Ramanathan CS;

FEDER J N. MINTIER G.

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25-APR-2003; 2003US-00424233
                                                                                                                           25-APR-2002; 2002US-0375335P
                                                                                                                                                                                          (RAMA/) RAMANATHAN C S.
                                                                                                                                                                                                                            Feder JN, Mintier G,
                                                                                                                                                                                                                                                             WPI; 2004-141759/14.
                             US2003220263-A1
Homo sapiens.
                                                           27-NOV-2003
                                                                                                                                                             (FEDE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                        The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. Luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                        response or sensitivity to troins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, particularly toxins and entibacterials useful as insecticides, particularly toxins and genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neural development disorder; apoptosis disorder; immune response disorder; dementia; anxiety; headache; migraine; delirium; schizophrenia; manic depression; mental retardation; dyskinesia; neural degenerative disorder; Alzheimers's disease; Parkinson's disease; depression; fear; learning disorder; brain cancer; gene therapy; human; nootropic; tranquilizer; neuroleptic; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                               Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                              Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leucine-rich repeat, LRR; HLRRNS-2; HLRRNS-3; aberrant leucine-rich repeat protein function disorder; protein: protein interaction disorder; matrix association disorder; caspase recruitment disorder; nucleotide binding disorder; cell migration disorder; signal transduction disorder; cell cycle regulation disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.2%; Score 46; DB 6; Length 190; 57.1%; Pred. No. 2.6; ive 2; Mismatches 4; Indels
                                                                             Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuron disorder; muscle development disorder;
                                                                                Frangeul L,
                                                                                                                                                                                                               Claim 2; SEQ ID NO 2822; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI36920 standard; protein; 635 AA.
                                                                              Glaser P,
                              (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
07-FEB-2001; 2001FR-00001659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 57.1%;
Conservative
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15 MGFGMTTILLNLHN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                Taourit S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human LRR protein #15.
                                                                                                                                WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 190 AA;
                                                                                               Buchrieser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-2004
                                                                                Duchaud E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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New isolated human leucine rich repeat containing polypeptides, HLRRNS-2 and HLRRNS-3, useful for treating, preventing disorders e.g., anxiety, headache, migraine, schizophrenia, manic depression, or delirium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimers's disease, Parkinson's disease affective disorders, depression, schizophrenia, anxiety, fear, learning disorders and brain cancer. The invention is also used in gene therapy. The present sequence is human LRR protein. The protein is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; immunestimulant; immunesuppressant; virucide;
antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                immune responses in the human nervous system such as dementia, anxiety, headache, migraine, delirium, schizophrenia, manic depression, severe mental retardation, dyskinesias, neural degenerative disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein clone nf56_3 protein sequence SEQ ID NO:132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Length 635;
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61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.8%; Score 42; DB 63.6%; Pred. No. 61; ive 4; Mismatches
                                                                               Example 1; SEQ ID NO 19; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY94963 standard; protein; 695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.
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432 GVSLSKLSLHN 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 635 AA;
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Matches
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New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity.
antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus, gradity versus-host-disease; autoimmune inflammatory eye disease; allergy.
                                                                                                                                                                                                                                                                                                              Collins-Racie LA, Evans C;
Steininger RJ, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 141; Page 592-594; 641pp; English.
                                                                                                                                                                                                                                                                                                             f, Lavallie ER, (
M, Agostino MJ,
Fechtel K;
                                                                                                                                                                                98US-0096622P.
98US-0092815P.
98US-0105368P.
99US-0115234P.
99US-01120575P.
99US-0120575P.
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                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                               Mccoy JM,
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                                                                                                                     WO200009552-A1.
                                                                                                  Homo sapiens.
                                                                                                                                                                                             17-AUG-1998;
04-SEP-1998;
23-OCT-1998;
08-JAN-1999;
12-FEB-1999;
18-FEB-1999;
                                                                                                                                                              13-AUG-1999;
                                                                                                                                          24-FEB-2000.
                                                                                                                                                                                                                                                          30-APR-1999;
                                                                                                                                                                                   14-AUG-1998
                                                                                                                                                                                                                                                                                                                          Merberg D,
Wong GG,
                                                                                                                                                                                                                                                                                                               Jacobs K,
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AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898 to AAA994980, isolated from human adult brain, adult thyroid, adult thyroid, adult cretina, foetal carcinoma, adult budd, adult thyroid, adult cattilage, kidney, foetal carcinoma, adult uterus, foetal tidney, does a dult cattilage, kidney, foetal bracenta, adult uterus, adult tumour, and brain, adult thyrois, foetal bracenta, adult uterus, adult tumour, and cadult bladder, cDNA libraries. The polymuclectides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polymuclectides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on southern gals, and so thromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined infections include human immunodeficiency virus (HIV), hepstitis, hepsesviruses, wycobacterial, bacterial, fungal and other candidiasis. The proteins and clicude used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus crythematosis, rheumatoid arthritis, autoimmune disorders and attritis, autoimmune disorders and altergic conditions, such asthma. AAA16598 to AAA16774 represent creat allergic conditions, such asthma. AAA16598 to AAA16774 represent creat allergic conditions, such asthma. Expectine sent invention

Sequence 695 AA;

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                                               Gaps
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Ouery Match

56.8%; Score 42; DB 3; Length 695;
Best Local Similarity 63.6%; Pred No. 67;
Matches 7; Conservative 4; Mismatches 0; Indels
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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide (I), its agoniat or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell factories of the invention have anti-inflammatory, anti-utoimmune and anti-diabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune-related diseases, particularly (i)-(iii). The products of the invention have anti-inflammatory, anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune-related diseases, particularly call-mediated diseases. The diseases treated include systemic lupus systemic sclerois (scleroderma), idopathic spondyloarthropathies, systemic sclerois, scleroderma), idopathic inflammatory myopathies (dermatomyositis, polymyositis), signament of inflammatory systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia chrombocytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia, thyroiditis (draws's disease, Hashimoto's thyroiditis, invenile lymphocytic thyroiditis (draws's disease, labahimoto's thyroiditis, mellitus, immune-mediated renal disease (glomerulonephritis).
                                                                                                                                                                                                                                                                                                 Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thyombocyclopenia; thyotoditis; diabetes mellitus; demyelinating polymeuropathy; cirrhosis; enteropathy; multiple sclerosis; polymeuropathy; polymeuropathy; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; whipple, s disease; skin disease; dermatitis; psoriaais; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition containing novel polypeptide PRO245, its agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;
                                                                                                                                                                                                                                                              Human PRO266 clone UNQ233 derived protein.
                                                                                                                                        AAY08076 standard; protein; 696 AA.
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97US-0059263P.
97US-0061550P.
97US-0065186P.
97US-0066364P.
97US-0066770P.
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492 GVSLSKLSLHN 502
4 GMALSKINLHN 14
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12-NOV-1997;
21-NOV-1997;
24-NOV-1997;
04-JUN-1998;
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Query Match 56.8%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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tubulointerstitial nephritis), multiple sclerosis, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary blilary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease. Crohn's disease, jutten-sensitive enteropathy, and Whipple's disease. Autoimmune or immune-mediated skin diseases including whipple's disease, erythema multiforme, contact dermatitis, psoriasis, bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis, asthma, allergic rhinitis, aropic dermatitis, food hypersensitivity, curticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases (graft rejection, and graft-versus-host-disease). (1), its (ant) agonists or fragment can also be used as an adjuvant in treatment of tumors. Antibodies against (I) can also be used as an adjuvant in treatment of tumors. This sequence represents a protein derived from human PRO266 clone UNQ233 CDNA which is described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of protein PRO266
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97US-0059115P.
97US-0059119P.
97US-0059121P.
97US-0059121P.
97US-0059263P.
97US-0059268P.
97US-0062285P.
97US-0062285P.
97US-00622814P.
97US-00622814P.
97US-0063814P.
97US-0063814P.
97US-0063814P.
97US-0063814P.
                                                                                                                                                                                                                                                                                                                                                                                   56.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Sequence 696 AA;
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15-OCT-1997;
17-OCT-1997;
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24-OCT-1997;
24-OCT-1997;
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21-0CT-1997
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AXY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal cDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal krain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known copypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the crepair of acute and chronic mucosal lesions (e.g. enterocolitis, copinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and edevelopment, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as a target for anti-tumor drugs. PRO533 may compered as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, con be used to treated tissue, e.g. in the heart of genital tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
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Pred. No. 67;
4; Mismatches 0; Indels
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                                                                 9705-0063541P.
9708-0063542P.
9708-0063549P.
9708-0063549P.
9708-0063564P.
9708-0063704P.
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9708-0063738P.
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9708-0064103P.
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24.0CT-1997;
27.0CT-1997;
27.0CT-1997;
28.0CT-1997;
28.0CT-1997;
28.0CT-1997;
28.0CT-1997;
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07-NOV-1
12-NOV-1
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Gaps

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Query Match
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/note= "Prokaryotic membrane lipoprotein lipid attachment
                                                                                                               PRO266; UNQ233; dermatological; immunosuppressive; antinflammatory; immunostimulant; antiasthmatic; antisheumatic; antiathritic; virucide; antiallergic; haemostatic; hepatotropic; antidiabetic; antianaemic; nephrotropic; neuroprotective; anticoagulant; immunological disorder; lung; preumonia; skin; psoriasis; kidney; glomearlonephritis; atthritis; appondiathry; slE; systemic lupus erythematosis; scleroderma; diopathic inflammatory myopathy; anaemia; thrombocytopenia; diabetes; thyrodidtis; Grave* a disease; demyelinating disease; multiple sclerosis; Grobn's disease; hepatobiliary disease; hepatobiliary disease; multiple sclerosis; graft-versus-host-disease;
                                                                                                                                                                                                                                                                  700.34
7note= "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                              note= "Casein Kinase II phosphorylation site"
?22. .226
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/hote= "Casein Kinase II phosphorylation site"
575. .599
                                                                                                                                                                                                                                                                                                                            /note= "cAMP and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                    Casein Kinase II phosphorylation site"
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note= "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                    "Casein Kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                            "N-myristoylation site"
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                                                 AAY70671 standard, protein; 696 AA.
                                                                                                                                                                                                                                                                                                               /note= "N _
.260 _
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/note= "N
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/note= ""
66
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/note= "N
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/note= "...
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/note= ""
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253. .257
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/note= "N-
                                                                                  18-JUL-2000 (first entry)
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|::|||::|||
493 GVSLSKLSLHN 503
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18. .22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                 Human PRO266 protein.
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Modified-site
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                                                                  AAY70671;
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The present sequence is the human protein PRO266, encoded by UNQ233 cDNA, designated as clone DNA37180. It is isolated from human foetal brain tissue. PRO266 has significant homology to a SLIT protein, indicating trissue. PRO266 has significant homology to a SLIT protein, indicating that it could be a leuchine rich repeat protein. It enhances or suppresses the infiltration of inflammatory cells into tissues, proliferation of T-I ymphocytes and modulates the immune response. This sequence is useful for treatment of immune related disorders, like SLB, rheumatoid/juvenile or treatment of immune related disorders, like SLB, rheumatoid/juvenile arthritis, spondyloarthropathy, systemic solerois (soleroderma), arthritis, arthrombocytropenia, thyroiditis e.g. Grave's disease, diabetes canaemia, thrombocytropenia, thyroiditis e.g. Grave's disease, diabetes mellitus, immune-mediated renal disease e.g. glomerulonephritis, demyelinating diseases such as multiple sclerosis and Guillain-Barre syndrome, hepatoblilary disease like hepatitis and primary biliary syndrome, hepatoblilary diseases like hepatitis and primary biliary cirrhosis, inflammatory and fibrotic lung diseases such as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or immune-mediated skin diseases such as sociated diseases such as safat. Persons and munological diseases con the lungs such as eosinophilic pheumonia and transplantation associated diseases such as graft-versus-host-disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for treatment and diagnosis of immune related diseases e.g. Grave's disease comprises a PRO245, PRO217, PRO301, PRO355, PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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608. .612

/note= "Casein Kinase II phosphorylation site"

646. .650

/note= "CaMP and cGMP-dependent protein kinase

phosphorylation site"

655. .659

/note= "Casein Kinase II phosphorylation site"

666. .670

/note= "Casein Kinase II phosphorylation site"

666. .670
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/note= "Casein Kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood WI;
note= "N-glycosylation site"
598. 604
note= "N-myristoylation site"
503. 609
                                                                                                                                  'note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 10; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US021547.
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98WO-US019437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fong S, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-271435/23.
N-PSDB; AAZ52205.
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17-SEP-1998;
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(first entry)

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Human, PRO, dermatological, antipsoriatic, cytostatic, antiinflammatory; antiparkinsonian nootropic, neuroprotective, vulnerary; cardiant; antiangiogenic, vasotropic, antiasthmatic, antirheumatic, cancer; antiarthitic, antiinfertility; antidiabetic, antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                                                                                                                                                                                                                                        22-FEB-2000; 2000WO-US004414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-2000; 2000WO-US000219
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                                                     Human PRO266 protein.
                                                                                                                                                                                                    WO200104311-A1.
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Filvaroff E, F
Godowski PJ, G
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Williams PM,
                                                                                                                                                                           Homo sapiens.
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02-DEC-1999;
                          24-APR-2001
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                                                                                                                                                                                                                             18-JAN-2001
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 AAB80227;
The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynuclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Bilison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, derma carring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, anglogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atterosclerosis, cardiac injury, infertility, premature aging, AlDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transagenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
                                                                                                                                antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neurotrophic; osteopathic; antiathmatic; antiarthritic; antirheumatic; antiarteriosclerotic; cardiant; antidabetic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartiage formation; angiogenesis; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AIDS; diabetes; stroke; gene therapy; transgenic; PRO; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO 91; 355pp; English.
                              ADC78411 standard; protein; 696 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   99WO-US021090.
                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US019330
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                              Human PRO266 protein.
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                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1998;
                                                                                  01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000.
                                                       ADC78411;
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Yuan J;
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99US-0145698P. 99US-0146222P. 99WO-US020594.

99WO-US021547.

99WO-US028214 99WO-US028564

99WO-US028313

99WO-US021090

99WO-US020944

99WO-US028565.

99WO-US030911 99WO-US030999

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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosoclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabbetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                    useful in the
                                                                                         Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 696;
67;
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Pred. No.
                                                                                                                                                                                                                                                                                          Claim 1; Fig 34; 393pp; English.
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2001-081051/09.
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Best Local Similarity
                                  N-PSDB; AAF72388
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Indels

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4; Mismatches

Best Local Similarity 63.6 Matches 7; Conservative

|::|||::||| GVSLSKLSLHN 503 4 GMALSKINLHN 14

493

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RESULT 15 AAB80227

AAB80227 standard; protein; 696 AA.

67;

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Ferrara N; ME, Goddard P Kljavin IJ; Tumas D;

L, Eaton DL, H, Gerritsen M Hillan KJ, F Stewart TA,

E, Fong S, Gao W, Gerber H, PJ, Grimaldi CJ, Gurney AL, F Pan J, Paoni NF, Roy MA, SM, Wood WI;

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Modified-site
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systemic lupus erythematosus; rheumatoid arthritis; systemic sclerosis;
yuvenile chronic arthritis; spondyloarthropathy; sjogren's syndrome;
idiopathic inflammatory; myopathy; polymyositis; systemic vasculitis;
yarcoidosis; autoimmune hemolytic anaemia; immune pancytopaenia;
yautoimmune thrombocytopaenia; fidiopathic thrombocytopaenia; principathic forave's disease; Hashimoto's thyroiditis; diabetes mellitus;
yautoimmune thrombocytopaenia; fidiopathic thrombocytopaenic purpura;
thyroiditis; Grave's disease; Hashimoto's thyroiditis; diabetes mellitus;
yauto inflammatory demyelinating disease; multiple sclerosis;
which inflammatory demyelinating polymeuropathy; infectious hepatitis;
wuto immune chronic active hepatitis; primary biliary cirrhosis;
yauto immune chronic active hepatitis; primary biliary cirrhosis;
yautoimmatory bowel disease; Crohn's disease; Whipple's disease;
yerythaemia multiforme; psoriasis; asthma; allergic rhinitis; urticaria;
yautoimpune disease; crohn's disease; immunogen;
yautoimpune dispathic preunonia; graft rejection;
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137. ...348
12 - ...
12 - ...
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  0; Indels
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/note= "Glycine is N-myristoylated"
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//note= "Asn is N-glycosylated"
465. .471
/note= "Glycine is N-myristoylated"
                                                                                                                                                                                                                                                                                  Human immune response protein PRO266 (UNQ233).
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/note= "Asn is N-glycosylated"
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  4; Mismatches
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16. .696
/label= Mature_PRO266
17. .23
/note= "Gl....
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/label= Signal_peptide
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                                                                                                                                                                     AAU00824 standard; protein; 696 AA.
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/note= ""
                                                                                                                                                                                                                                               04-JUL-2001 (first entry)
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/note= "As
302. . 308
/note= "G1
7; Conservative
                                                            493 GVSLSKLSLHN 503
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                                                                                                                                                                                                          AAU00824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody.
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  Matches
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The sequence represents Human PRO266 (UNQ233), a protein involved in the immune response. PRO polypeptides, and (ant)agonists to them, are used in compositions for modulating infiltration of inflammatory cells into a cissue, modulating an immune response and modulating proliferation of tissue, modulating an immune response and modulating proliferation of T. Insue, modulating an immune response and modulating proliferation of T. Insue, modulating an immune related diseases can be treated with the compositions, such as, systemic lupus erythematosus, compositions, such as, systemic slopathic inflammatory composities, systemic sclerosis, idopathic inflammatory autoimmune haemolytic anaemia (e.g. immune pancytopaenia).

CC myopathies (e.g. Grave's disease, Hashimoto's thyroiditis), diabetes molitus, immune-mediated renal disease (e.g. immune pancytopaenia).

CC myopathies (e.g. Grave's disease, Hashimoto's thyroiditis), diabetes melitus, immune-mediated renal disease (e.g. immune pancytopaenia).

CC myopathiating polymoropathy, hepatobilary diseases such as infectious demyelinating polymeuropathy, hepatobilary diseases such as infectious demyelinating polymeuropathy, hepatobilary diseases such as infectious demyelinating polymeuropathy, hepatobilary diseases such as infectious diseases (ulcerative colitis, Crohn's disease (e.g. erythemenia multiforme and psoriasis), asthma allergic rhinitis, urticaria, food hypersensitivity, immune-mediated skin diseases (e.g. erythemenia multiforme confinence of immune-mediated skin diseases (e.g. erythemenia multiforme proteomenials), asthma allergic rhinitis, urticaria, food hypersensitivity, immunologic disease and whipple's diseases, of the lumg such as eosinophilic promeomias, idiopathic pulmonary fibrosis, transplantation associated configures and to stimulate the proliferation of T lymphocytes. Anti-PRO inhibitors, and to estimulate the proliferation of T lymphocytes, and to estimulate the proliferation of T lymphocytes antibodies can be used to detect PRO and in diagnosis p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for diagnosing and treating immune related diseases, e.g. rheumatoid arthritis and diabetes mellitus, comprises a PRO polypeptide, agonist, antagonist or fragment.
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493. .499
/note= "dlycine is N-myristoylated"
595. .599
/note= "Asn is N-glycosylated"
598. .604
/note= "Glycine at 598 is N-myristoylated"
603. .609
/note= "Glycine is N-myristoylated"
619. .639
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 4; Length 696;
Pred. No. 67;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                           555. .659
/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2000; 2000WO-US007377.
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Best Local Similarity 63.0-
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493 GVSLSKLSLHN 503
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N-PSDB; AAS00160.
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                                                                            Modified-site
                                                                                                                                                 Modified-site
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AAU12348;

RESULT 17 AAU1234

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AMU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to and to detect the presence of mammalian lung, colon, polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO colypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour of the 275 sequences are also useful to stimulate the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of reprinted to finner ear utricular supporting cells or of repression, or the proliferation of endothelial cells. Some of the PRO (PBMCS), or the proliferation of endothelial cells. Some of the PRO colypeptides may modulate glucose or free faity acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor involved in binding interactions. The prolifers encoding PRO colypeptides can be used in assays to identify molecules involved in binding interactions. The prolymoclecides encoding PRO colypeptides can be used to generate probes, antisense RNA/DNA,
    Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 696;
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                                                                                                            Claim 12; Fig 354; 813pp; English
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99US-0144732P.
99US-0144758P.
99US-0146222P.
99WO-US021011.
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99US-0162506P
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493 GVSLSKLSLHN 503
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15-SEP-1999;
15-SEP-1999;
29-OCT-1999;
30-NOV-1999;
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20-JUL-1999;
20-JUL-1999;
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Matches
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                                                                                                                                                                                                                           Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                            AAU12348 standard; protein; 696 AA
                                                                                                                                                                                             Human PRO266 polypeptide sequence.
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11. FEB - 2000; 2000WO-US003565.
11. FEB - 2000; 2000WO-US00341.
11. FEB - 2000; 2000WO-US004414.
12. FEB - 2000; 2000WO-US004414.
13. FEB - 2000; 2000WO-US004914.
14. FEB - 2000; 2000WO-US005601.
15. MAR - 2000; 2000WO-US005601.
15. MAR - 2000; 2000WO-US005601.
15. MAR - 2000; 2000WO-US00581.
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2000WO-US015264.
2000US-0209832P.
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99WO-USO28551.
99WO-USO28564.
99WO-USO28565.
99US-0170262P.
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2000WO-US000219.
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2000WO-US008439.
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                                                                                                                                                       (first entry)
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Gerritsen ME, Goddard Smith V, Stewart TA,
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21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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30-MAY-2000;
02-JUN-2000;
05-JUN-2000;
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Gaps

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ABU71605 standard; protein; 696 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;
Watanabe CK, Wood WI;
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01-DEC-1999; 99WO-US028634.
02-DEC-1999; 99WO-US0228551.
09-DEC-1999; 99WO-US0225651.
09-DEC-1999; 99WO-US022565.
09-DEC-1999; 99WO-US020565.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US0044114.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US0049114.
24-FEB-2000; 2000WO-US0049114.
24-FEB-2000; 2000WO-US0049114.
24-FEB-2000; 2000WO-US0049114.
24-FEB-2000; 2000WO-US0049114.
24-FEB-2000; 2000WO-US005611.
24-FEB-2000; 2000WO-US005611.
25-MAR-2000; 2000WO-US005811.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US007532.
31-MAR-2000; 2000WO-US007532.
31-MAR-2000; 2000WO-US007532.
31-MAR-2000; 2000WO-US007532.
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Best Local Similarity 63.6
Matches 7; Conservative
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N-PSDB; AAC91464.
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Human, PRO; secreted polypeptide; transmembrane polypeptide; pathological disorder; protein secretion; pathological disorder; protein secretion; pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antidiabetic; dermatological; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9705-0059113P
9705-0059113P
9705-0059113P
9705-0059121P
9705-0059124P
9705-0059124P
9705-0059263P
9705-0062287P
9705-0062287P
9705-0062287P
9705-0062314P
9705-0062314P
9705-0063121P
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9705-0063124P
9705-006354P
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97US-0063870P.
97US-0064248P.
97US-0064248P.
97US-0065186P.
97US-0065186P.
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97US-0066466P.
97US-0066511P.
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                                                                          16-JUN-2003 (first entry)
                                                                                                                 Human PRO polypeptide #16
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24-NOV-1997;
24-NOV-1997;
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17-OCT 1997

24-OCT 1997

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27-OCT 1997

28-OCT 1997

29-OCT 1997

20-OCT 1997

20-OC
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                                  ABU71605;
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Gaps ; 0

> GVSLSKLSLHN 503 GMALSKINLHN 14

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Human; secreted and transmembrane protein; PRO; antiinflammatory;
                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO266.
                                                                                                                              AB017792 standard; protein; 696 AA.
                                                                                                                                                                                                                                          (first entry)
493 GVSLSKLSLHN 503
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29-OCT-1998;
20-NOV-1998;
01-DEC-1998;
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20-APR-1999;
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02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
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ME, Goddard A;
Kljavin IJ;
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02-MAR-2000; 2000WO-US005841.

20-MAR-2000; 2000WO-US007377.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

02-UJN-2000; 2000WO-US014042.

28-JUL-2000; 2000WO-US015564.
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antiatreriogolerotic, cardiant; anti-infernility, anti-HIV; cytostatic; antidabetic; gene therapy; tumour necrosis factor (TNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease, organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; blosensor; bloreactor; tissue typing.
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Gaps

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56.8%; Score 42; DB 6; Length 696; 63.6%; Pred. No. 67; ive 4; Mismatches 0; Indels

Best Local Similarity 63.6 Matches 7, Conservative

Query Match

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Claim 12; Fig 354; 660pp; English.

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11 FEB - 2000; 2000MC-USOUS.

12 FEB - 2000; 2000MC-USOUS.

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15 FEB - 2000; 2000MC-USOUS.

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WPI; 2003-341980/32. N-PSDB; ACD24029.

New secreted and transmembrane PRO nucleic acids, for treating inframmation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (ALDS), or cancer.

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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding collaboration in the specification. The polypeptide encoded by (I) is used to are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a biological activity of a cell, stimulate the release of twoour necrosis factor (TMP) alpha from human blood, modulate the proliferation or differentiation of cells or gene expressing to the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide companies of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inframmatory diseases, organ failure, archivosclerosis, cardiac injury, infertility, diseases, organ failure, and acquired immunodeficiency syndrome (ADS), cancer, or diabetic complications. The nucleic acid is useful as the nucleic acid is useful as the amino acid sequence of a novel human secreted and treasure typing. This is the amino acid sequence of a novel human secreted and
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Ferrara N; 1 ME, Goddard A; Kljavin IJ; Tumas D; , Botstein D, Desnoyers L, Eaton DL, I Fong S, Gao W, Gerber H, Gerritsen I Grimaldi JC, Gurney AL, Hillan KJ, I Pan J, Paoni NF, Roy MA, Stewart TA, Wood WI; Ashkenazi A, Filvaroff E, Godowski PJ, Mather JP, P? Williams PM,

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                                                                                                                                     The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisanse RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals oknock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's disease or ischaemia, and in various diagnostic assays. ABU71445-ABU71505 represent human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; diabetes; bone disorder; cartilage disorder; rheumatoid arthritis; obesity; sports injury, osteoarthritis; hyper-insulinaemia; hypo-insulinaemia; hearing loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic.
                                           New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      56.8%; Score 42;
63.6%; Pred. No. 6
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                                                                                                                Claim 12; Fig 34; 474pp; English
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97US-0056974P.
97US-0059113P.
97US-0059117P.
97US-0059124P.
97US-0059184P.
97US-0059352P.
97US-0059382P.
97US-0059388P.
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les 7, Conservative
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WPI; 2003-361832/34.
N-PSDB; ACAS8367.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 696 AA;
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17-0CT-1997;
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97US-0063128P
97US-0063174P
97US-0063714P
97US-0063714P
97US-0063714P
97US-0063714P
97US-006314P
97US-0065846P
97US-0065846P
97US-0065846P
97US-0065848P
97US-0071288P
98US-007128P
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99WO-US030095.
99WO-US030911.
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98WO-US022991.
98WO-US022992.
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98WO-US025108.
99WO-US000106.
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99WO-US020944
117 OCT 11997

124 OCT 11997

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The present invention relates to the isolation of novel human PRO polypoptides, and the polynuclectide sequences encoding them. The PRO polypoptides are secreted and transmembrane proteins. The PRO polypoptides and polynuclectides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinamenia, hearing loss, and cosquiation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or or netwal sources. Asugos7-Abusil44 represent the human PRO or netwal sources. Asugos7-Abusil44 represent the human PRO set the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence at a supposition at the patent of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 354; 643pp; English.
20-DEC-1999; 99WO-US030999.
30-DEC-1999; 99WO-US031274.
50-DEC-1999; 99WO-US031274.
65-JAN-2000; 2000WO-US000219.
66-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US00376.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US004314.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US006914.
24-FEB-2000; 2000WO-US006914.
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Best Local Similarity 63.6
Matches 7; Conservative
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N-PSDB; ACA67170.
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ABU71906
ABU71906
ABU71906
AC ABU7
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9705-0063544P

9705-0063549P

9705-0063564P

9705-0063764P

9705-0063732P

9705-0063734P

9705-0063734P

9705-0063734P

9705-0063748P

9705-0063748P

9705-0063748P

9705-0064103P

9705-0064103P

9705-0064103P

9705-006418P

9705-006418P

9705-006418P

9705-006418P

9705-006618P

9705-006618P

9705-006618P

9705-0066120P

9705-006618P

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9705-006618P
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99WO-US030999.
2000WO-US000219.
2000WO-US003565.
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97US - 0062816P.
97US - 0063120P.
97US - 0063121P.
97US - 0063127P.
97US - 0063128P.
97US - 0063329P.
97US - 0063329P.
97US - 0063329P.
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98WO-US019177.
98WO-US019330.
98WO-US019437.
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99WO-US020594.
99WO-US020944.
                             97US-0059113P.
97US-0059117P.
97US-0059117P.
97US-0059121P.
97US-0059122P.
97US-0059184P.
97US-0059263P.
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97US-0062285P.
97US-0062287P.
97US-0063486P.
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              2001US-00904011
               11-JUL-2001;
                                                                                    18-SEP-1997;
18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
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28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
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28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
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21-OCT-1997;
24-OCT-1997;
24-OCT-1997;
                             17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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29-NOV-1999
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15-SEP-1999
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17-SEP-1997
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17-NOV-19
18-NOV-19
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The invention relates to an isolated nucleic acid with at least 80% concleic acid sequence identity to a nucleotide sequence encoding one of concleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or RPO polypeptides or encoding a CC the PRO nucleic acid, a host cell for the expression of the RPO collypeptide (by culturing the host cell for the expression of the RPO polypeptide (paving at least 80% sequence identity to: (c) an isolated PRO polypeptide (having at least 80% sequence identity to: (c) an isolated PRO polypeptide (having at least 80% sequence identity to: (d) an amino acid sequence selected from the ofly propertied (b) an amino acid sequence selected from the objection); or (c) an extracellular domain of acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of acid sequence amino acid sequence, an anti-PRO antibody, detecting a peptide), a chimaeric molecule comprising a PRO polypeptide of to a cheerologous amino acid sequence, an anti-PRO antibody, detecting a percent and sample suspected of containing the polypeptide, or Indianal acidity of a cell expressing a PRO245 or PRO1868 and containing the polypeptide and acids which encode PRO can be used to generate either transgent annians or knock-out animals which may be used in the conformation and screening of therapeutically useful reagents. The nucleic acids may also be used in the proposent adants and the isolated cuseful as molecular markers for protein electrophoresis, and the isolated cuseful as molecular markers for protein electrophoresis, and the isolated cuseful as molecular markers for protein electrophoresis, and the isolated cuseful as molecular markers for protein electrophoresis, and the isolated cuseful as molecular markers for protein electrophoresis, and the isolated sources. The proposite representes a PRO polypeptide are useful in diagnostic assays for PRO polypeptide and and acide may al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
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                                                                                                                                                                                                                                                                              Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;
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Pred. No. 67;
4; Mismatches
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63.6%; Pred
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                    24-FEB-2000; 2000WO-US005004.

02-WAR-2000; 2000WO-US005841.

20-WAR-2000; 2000WO-US004377.

30-WAR-2000; 2000WO-US004439.

22-MAY-2000; 2000WO-US014042.

02-UTN-2000; 2000WO-US015564.

28-UTL-2000; 2000WO-US012328.

18-SEP-2000; 2000WO-US023328.
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493 GVSLSKLSLHN 503
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22-FEB-2000;
24-FEB-2000;
20-MAR-2000;
30-MAR-2000;
31-MAR-2000;
22-MAY-2000;
22-UN-2000;
28-JUL-2000;
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Matches
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AB001789

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07-AUG-2003 (first entry)
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17-88P-1997;
17-88P-1997;
17-88P-1997;
17-88P-1997;
17-88P-1997;
17-88P-1997;
18-88P-1997;
18-88P-1997;
18-88P-1997;
18-88P-1997;
18-88P-1997;
18-88P-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
25-0CT-1997;
26-0CT-1997;
28-0CT-1997;
28-0C
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24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
10-SEP-1998;
14-SEP-1998;
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Human, secreted and transmembrane protein; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; Parkinson's disease; hallammation; nepkinson's disease; inflammation; nepkintis; wound healing; nerve repair; collateral blood vessel formation; cancer; colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes; cirrhossis; fibrosis; dermal fibrotic condition; keloid; scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis; infertility; gene therapy. Novel human secreted and transmembrane protein PRO266. 9705-0059113P 9705-0059113P 9705-0059113P 9705-0059113P 9705-0059121P 9705-0059121P 9705-0059121P 9705-0059121P 9705-0059121P 9705-0059121P 9705-005914P 9705-005914P 9705-005914P 9705-005912P 9705-005912P 9705-005912P 9705-005912P 9705-005912P 9705-005914P 17-JUL-2001; 2001US-00907824

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16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019330.
08-SEP-1999; 98WO-US025108.
08-SEP-1999; 99WO-US025108.
15-SEP-1999; 99WO-US020594.
15-SEP-1999; 99WO-US021547.
25-NOV-1999; 99WO-US021547.
02-DEC-1999; 99WO-US02814.
02-DEC-1999; 99WO-US02814.
02-DEC-1999; 99WO-US02865.
02-DEC-1999; 99WO-US02866.
02-DEC-1999; 99WO-US02864.
02-DEC-1999; 99WO-US0399.
02-MAR-2000; 2000WO-US0034377.
02-MAR-2000; 2000WO-US039388.
02-JUN-2000; 2000WO-US039388.
02-JUN-2000; 2000WO-US039388.
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-370793/35. N-PSDB; ACD07474.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO315), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.

Claim 12; Fig 34; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-1119 amino acids fully defined in the specification. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. Parkinson's disease, particularly useful for detecting or treating e.g. Parkinson's disease, c.g. Alzheimer's disease, inflammations, nephritis, wound healing, nerve capair, collateral blood vessel formation, cancers (e.g. colorectal cancer) the memorinage (or reduce risk for haemorinage), rheumatoid canceri, haemorinage (or reduce risk for haemorinage), in the colorectal conditions (e.g. keloids or scarring), restenosis, dermal fibrotic conditions (e.g. keloids or scarring), or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or the presence of these diseases, and diagnostic determination of the presence of these diseases, and diagnostic determination of the presence of these diseases, and diagnostic determination of the presence of the mannal stables are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO polypeptides are useful as the amino content of a novel human secreted and transmembrane PRO polypeptide.

Sequence 696 AA;

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Claim 12; Fig 354; 660pp; English
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             Gaps
                                                                                                                    Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
             ö
Score 42; DB 6; Length 696;
Pred. No. 67;
4; Mismatches 0; Indels
                                                                     ABU66746 standard; protein; 696 AA
                                                                                                                                                                                                                                           98WO-US019177.
98WO-US019330.
98WO-US019437.
98WO-US021141.
98WO-US022991.
98WO-US0224855.
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99WO-US005028.
99WO-US005190.
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99WO-US010733.
99WO-US012252.
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99WO-US021090.
99WO-US021547.
99WO-US023089.
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99WO-US028313.
99WO-US028409.
99WO-US028301.
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98WO-US019093.
98WO-US019094.
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99WO-US031274.
2000WO-US000219.
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                                                                                                                                                                                    09-MAY-2002; 2002US-00143114
Query Match 56.8%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                          Human PRO polypeptide #177.
                                                                                             23-MAY-2003 (first entry)
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493 GVSLSKLSLHN 503
                         4 GMALSKINLHN 14
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30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
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28-ANG-1998
14-SEP-1998
14-SEP-1998
14-SEP-1998
16-SEP-1998
17-SEP-1998
17-SEP-1998
29-OCT-1998
29-OCT-1998
20-NOV-1998
01-DEC-1998
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08-MAR-1999;
10-MAR-1999;
20-APR-1999;
14-MAY-1999;
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13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
                                                                                                                                                Homo sapiens.
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                                                                                 ABU66746;
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001MO-US006666.
2001US-00802706
2001US-00808689.
2001US-0081544.
2001US-00854208.
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2001US-00860216.
2001US-00866038.
2001US-00866034.
2001US-00872035.
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2000MO-US013705.
2000MO-US014042.
2000MO-US014941.
2000MO-US015264.
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2000US-00747259.
2000WO-US034956.
2001US-00796498.
                                             2000WO-US004342.
2000WO-US004414.
2000WO-US004914.
2000WO-US005004.
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2000WO-US023328.
2000WO-US030952.
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2001US-00887879
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2001US-00931836
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19-DEC-2001; 2001US-00028072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-332040/31.
N-PSDB; ACA03779.
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14-JUN-2001;
19-JUN-2001;
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28-JUL-2000;
11-AUG-2000;
24-AUG-2000;
08-NOV-2000;
01-DEC-2000;
20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
28-FEB-2001;
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05-APR-2001;
10-MAY-2001;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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15-MAR-2000;
20-MAR-2000;
21-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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18-MAY-2001;
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01-JUN-2001;
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29-JUN-2001;
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Gao W;

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The present invention relates to the isolation of novel human PRO polypeptides, and the polymucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating consistent of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides, and for for cells expressing PRO polypeptides are useful for for stimulating the proliferation or differentiation of chuman blood, for stimulating the proliferation or differentiation of chomorocytes, and detecting the proliferation of antisense RNA and condrocytes, and detecting the prosence of tumours. The polymicleotide condrocytes, and detecting the prospetides, for generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation and transgenic consists of patent was obtained in gene therapy. ABU66570-ABU66844 represent the human PRO polypeptides of the invention. Note: The sequence data for this center sequence data for this are sequence data for this at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PRO, secreted protein, transmembrane protein; enterocolitis; gastrointestinal ulceration; skin disease; absorval kerationcyte differentiation; psoriaais; epithelial cancer; squamous cell carcinoma; Alzheimer's disease; Parkinson's disease; anyotrophic lateral sclerosis; inflammatory disease; arheumatoid arthritis, asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AlDS; acquired immunodeficiency syndrome; cancer; diabetic complication; wound repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.8%; Score 42; DB 6; Length 696; Best Local Similarity 63.6%; Pred. No. 67; Matches 7; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein PRO266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU54362 standard; protein; 696
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970S-0059113P.
970S-0059117P.
970S-0059121P.
970S-0059121P.
970S-0059184P.
970S-0059184P.
970S-0059184P.
970S-0059184P.
970S-0059184P.
970S-0063185P.
970S-0063185P.
970S-0063186P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 GVSLSKLSLHN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMALSKINLHN 14
                                                                                                                                                                                                                                                                                                                                                      Sequence 696 AA;
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17-SEP-1997,
17-SEP-1997,
17-SEP-1997,
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RR 24-CCT-1997; 9703-0061026P.
RR 24-CCT-1997; 9703-006112P.
RR 24-CCT-1997; 9703-006112P.
RR 24-CCT-1997; 9703-006112P.
RR 24-CCT-1997; 9703-006112P.
RR 24-CCT-1997; 9703-006132P.
RR 24-CCT-1997; 9703-006132P.
RR 24-CCT-1997; 9703-006132P.
RR 26-CCT-1997; 9703-006134P.
RR 26-CCT-1997; 9703-006613P.
RR 27-CCT-1997; 9703-006613P.
RR 27
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99US-0143048P
                                                       US2003044839-A1.
                   Homo sapiens.
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29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
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24-OCT-1997;
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17-OCT-1997;
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24-NOV-1997;
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oldsymbol{x}
                                                                                                                                                                                         The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequences given in the specification (depearing as ABU94347- adid sequences given in the specification); (c) an amino acid sequence encoded by the nucleotide sequence approach in the specification); (c) any one of the PRO sequences which its associated signal peptide; of (e) an extracellular domain of the PRO polypeptide with its associated signal peptide; or (e) an extracellular domain of the PRO polypeptide with its associated signal peptide; or (e) an extracellular domain of the PRO polypeptide with its associated signal peptide. Also include are the nucleic acids encoding the PRO polypeptides where the nucleic acids encoding the PRO polypeptides and nucleic acids are useful in diagnosing or treating entercoolitis, gastrointestinal ulceration, skin diseases associated with cancers such as squamous cell carcinoma, Alzheimer's disease, PADA and ADA as squamous cell carcinoma, Alzheimer's disease, e.g. cancers such as squamous cell carcinoma, Alzheimer's disease, e.g. cheumatoric artheritis, asthma or multiple sclerosis, organ failure, athematory diseases, e.g. cancers such as squamous cell carcinoma, Alzheimer's disease, permature concerned with re-growth of tissue. The nucleotide sequences may be used to polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used concerned with re-growth of tissue. The nucleotide sequences may be used concerned with re-growth of tissue. The nucleotide sequences may be used to bolypeptides, in assays to identify other proteins or molecules involved tissue to probes in chromosome and gene mapphing, or in generate transgenic and molecules are also useful in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and cissues purposes. The anti-PRO antibodies may be used in diagnostic assays f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, abnormal bleeding; gynaecological disease; asthma; hysterectomy; anglogenesis; coronary ischaemic condition; skin disease; asterial mucosa disorder; acute mucosal lesion; neuropathy; ALS; chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; uncortrolled cell growth, cancer; blood cosqulation cascade; thrombosis; haemorrhage; endometrial bleeding; anglogenesis; wound healing; tumour; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
                                                       New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.8%; Score 42; DB 6; Length 696; 63.6%; Pred. No. 67; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane polypeptide PRO266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO47377 standard; protein; 696 AA.
                                                                                                                                                                Claim 12; Fig 34; 473pp; English.
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493 GVSLSKLSLHN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
WPI; 2003-147434/14.
N-PSDB; ABX71522.
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                                                                                                                           disease.
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AB047377

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970S-0059113P.
970S-0059113P.
970S-0059111P.
970S-0059121P.
970S-0059121P.
970S-0059121P.
970S-0059285P.
970S-00628285P.
970S-0062814P.
970S-0062814P.
970S-0062814P.
970S-0063814P.
970S-0063812P.
970S-0063812P.
970S-0063812P.
970S-0063812P.
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970S-0063814P.
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98WO-US018824
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98US-0113296P
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10-JUL-2001; 2001US-00902903
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RESTUL-1999; 9908-0145639P.

RESTRATES STATES STATE
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Human, PRO; hypertrophy of neonatal heart; angiogenesis, wound healing, cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial acl growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chondrocyte proliferation; crown's disease; chondrocyte proliferation; sports injury; arthritis.
                                             Gaps
                                           ö
                     6; Length 696;
                                           0; Indels
                                                                                                                                                                                                                  Novel secreted and transmembrane protein PRO266
                     Score 42; DB 6
Pred. No. 67;
4; Mismatches
                                                                                                                                               ABU59827 standard; protein; 696 AA.
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9WO-US014552

9WO-US014552

9WO-US01803

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99WO-US028634
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                                 .68;
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                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                               493 GVSLSKLSLHN 503
                                                                  4 GMALSKINLHN 14
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Sequence 696 AA;
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08-MAR-1999;
10-MAR-1999;
20-APR-1999;
14-MAY-1999;
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DEC-1998;
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12-JUN-1998;
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99WO-US030095.
99WO-US030911.
99WO-US030999.
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22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
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2001US-00866028.
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2001US-00874503.
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19-DEC-2001; 2001US-00028072
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                                                                2000WO-US000219
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      99WO-US028564
99WO-US028565
                                          99WO-US030720
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25-MAY-2001; 2
25-MAY-2001; 2
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10-MAY-2001;
18-MAY-2001;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
22-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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01-MAR-2000;
02-MAR-2000;
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08-NOV-2000;
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 oldsymbol{X}
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Gao W;
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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US2003036179-A1 Homo sapiens,

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO cin modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 ctimulate adrenal cortical capillary endothelial growth, and PRO516, PRO143, PRO828, PRO826, PRO826, PRO826, PRO9156, PRO943, PRO828, PRO826, PRO1164 and PRO1186 or pro943, PRO828, PRO826, PRO1164 and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular cancerous tumours. PRO812 inhibits vascular cancerous tumours. PRO812 inhibits wascular candathelial growth factor (WESF) stimulated proliferation of endothelial coll growth factor (WESF) stimulated proliferation of candathelial growth and PRO136 and PRO136 or Collection of mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO136 or PRO132 is also enhances survival/proliferation of immune response. PRO828, PRO826, PRO132 is also enhances survival/proliferation of disorders of injuries, e.g. retinitis pigmencosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammals whichey mesangial cells, and therefore are useful for treating vich as Berger disease or other nephropathies associated with dermatitis, herpetiformis or culture and are thus useful for treating sports injuries, and arthritis. This is the mino acid sequence of a novel human PRO protein ö Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood; proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell; PBMC; glucose upcake; FRA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell; A-peptide; factor VIIA. Gaps ö Score 42; DB 6; Length 696; Pred. No. 67; 4; Mismatches 0; Indels Human secreted/transmembrane protein (PRO) #177. ABO25017 standard; protein; 696 AA. Claim 12; Fig 354; 659pp; English 56.8%; 05-SEP-2003 (first entry) Best Local Similarity 63.6 Matches 7; Conservative |::|||::||| 493 GVSLSKLSLHN 503 GMALSKINLHN 14 WPI; 2003-148238/14. N-PSDB; ABX89317. Sequence 696 AA; AB025017; 4 Query Match RESULT 29 AB025017 8 셤

us-10-769-514-17.rag

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99WO-US012223
99WO-US020344
99WO-US020344
99WO-US020313
99WO-US021547
99WO-US021547
99WO-US0215409
99WO-US0215409
99WO-US0215409
99WO-US0215409
99WO-US0215409
99WO-US02113
99WO-US0211243
99WO-US0211244
99WO-US02124441
                                                      97WO-US005230.
98WO-US011455.
98WO-US011452.
98WO-US0118824.
98WO-US0119093.
98WO-US0119093.
98WO-US0119077.
98WO-US0119177.
98WO-US011417.
98WO-US021911.
98WO-US022991.
98WO-US022992.
99WO-US022108.
99WO-US021108.
                            10-MAY-2002; 2002US-00142431
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2000WO-US032678
                                                                                    14-70L-1998;
14-50L-1998;
16-60L-1998;
16-60L-1999;
16-60
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20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
09-MAR-2001; 2001WO-US00666.
09-MAR-2001; 2001US-00806689.
14-MAR-2001; 2001US-00806689.
15-MAR-2001; 2001US-00806689.
10-MAY-2001; 2001US-00866216.
10-MAY-2001; 2001US-00866216.
25-MAY-2001; 2001US-0086634.
25-UW-2001; 2001US-0087879.
27-UW-2001; 2001US-00887879.
28-UW-2001; 2001US-009287796.

(GETH) GENENTECH INC.

3 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerriten ME, Goddard A, Godowski Pr, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watenabe CK, Wood WI, Zhang Zi,

WPI; 2003-466355/44. N-PSDB; ACD41971.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 of PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.

Claim 12; Fig 354; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) CDNA comprising a nucleic acid (a) encoding a PRO polypepide, or its comprising a nucleic acid (a) encoding a PRO polypepide, or its comprising any of the 275 120-850 residue amino acid sequences, comprising any of the 275 300-3500 nucleotide sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences given in the specification, or of the DNA deposited under any of the American Type (a) properties of the DNA deposited under any of the American Type (a) properties of a properties of the DNA deposited under any of the American Type (a) properties detailed above, a chimacian inscribed, the isolated PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, simulating the release of tumour necrosis (actor-alpha TYMF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood enonuclear cells (PBNC), and peripheral prome peripheral blood enonuclear cells (PBNC), and peripheral prome peripheral blood enonuclear cells (PBNC), and peripheral proferention of inner ear utricular supporting cells (or prolliferation of inner ear utricular supporting cells (or prolliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endochtellal earls), inhibiting the binding of A-peptide to factor villa, or differentiation of adipocyte cells, or of endochtellal cells, inhibiting the presence of a tumour in a mammal and an and an acid process.

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Claim 12; Fig 34; 477pp; English
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in the specification. The polymucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polymucleotide may also be used in preparing PRO polymptides by recombinant techniques, and in generating either transgenic animals knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polyment animals antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence rperseents a PRO
                                                                                                                                                                                                                                                                                                                  Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; therapeutic; hyperplasia; endometriosis; cancer; tumour; ischaemia; coronary arterial disease; polycystic kidney disease; renal failure; inflammatory response; asthma; rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy; cytostatic; gynecological; cardiant; nephrotropic; hepatotropic; antiinflammatory.
                                                                                                                                                             Gaps
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                                                                                                                                         6; Length 696;
                                                                                                                                                            0; Indels
                                                                                                                                         Score 42; DB 6
Pred. No. 67;
4; Mismatches
                                                                                                                                                                                                                                                                                                    Human secreted/transmembrane protein, #18.
                                                                                                                                                                                                                                               ABU64514 standard; protein; 696 AA.
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970S-0059117P-
970S-0059121P-
970S-0059128P-
970S-0059263P-
970S-0059266P-
970S-0062285P-
970S-0062285P-
970S-0062287P-
970S-006328P-
970S-006328P-
970S-006312P-
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                                                                                                                                         56.8%;
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                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                    Query Match
Best Local Similarity 63.6'
                                                                                                                                                                                          |::|||::|||
GVSLSKLSLHN 503
                                                                                                                                                                               4 GMALSKINLHN 14
                                                                                                                          Sequence 696 AA;
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15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
24-OCT-1997;
24-OCT-1997;
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24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2001;
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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                                                                                                         polypeptide
                                                                                                                                                                                                                                                                 ABU64514;
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New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease
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ME, Goddard A;
Kljavin IJ;
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97US-0063549P.
97US-0063550P.
97US-0063435P.
97US-0063734P.
97US-0063734P.
97US-0063734P.
97US-0063738P.
97US-0063738P.
97US-0063748P.
97US-0063870P.
97US-0064809P.
97US-0065846P.
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2000WO-US005841.
2000WO-US007377.
2000WO-US008439.
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98WO-US019330.
98WO-US019437.
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2000WO-US004414.
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99WO-US020594
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Filvaroff E, Fong S, Gao
Godowski PJ, Grimaldi JC,
Mather JP, Pan J, Paoni
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20-MAR-2000;
30-MAR-2000;
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22-FEB-2000;
24-FEB-2000;
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 28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
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31-0CT-1997;
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Ashkenazi A,
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           The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide, for linking at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. hyperplasis, endometriosis, cancers (e.g. those involving solid tumours), ischaemia, coronary arterial disease, polycystic kidney disease, chronic or acute renal failure, or inflammatory responses (e.g. asthma, theumatorid arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may gene. The sequences presented in ABUG4499-ABUG4559 are the PRO polymucleotides of the invention
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AC ABU67360;

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XX Buman gene therapy; mucosal lesion; v

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X Human; gene therapy; mucosal lesion; v

X Homo saplens.

XX A Homo saplens.

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| GVSLSKLSLHN 503
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Matches 7;
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PR 28-0CT-1997; 97UG-0063541P
PR 28-0CT-1997; 97UG-0063542P
PR 28-0CT-1997; 97UG-0063544P
PR 28-0CT-1997; 97UG-0063544P
PR 28-0CT-1997; 97UG-0063544P
PR 29-0CT-1997; 97UG-0063546P
PR 29-0CT-1997; 97UG-0063546P
PR 29-0CT-1997; 97UG-0063134P
PR 11-0CT-1997; 97UG-0063134P
PR 11-0CT-1997; 97UG-0063134P
PR 12-0CT-1997; 97UG-006314P
PR 12-0CT-1997; 97UG-006514P
PR 12-0CT-1997; 97UG-0066314P
PR 12-0CT-1999; 97UG-0103014P
PR 12-0CT-1999; 97UG-0103019P
PR 12-0C
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Ferrara N;

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Eaton

Desnoyers L,

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Botstein

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9705-0062125P.
9705-0062285P.
9705-00623814P.
9705-0063142P.
9705-00631212P.
9705-0063122P.
9705-0063122P.
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9705-0063122P.
9705-0063124P.
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9705-006423P.
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20-DEC-1999;
20-DEC-1999;
05-JAN-2000;
11-FEB-2000;
               15-0CT-1997;
17-0CT-1997;
21-0CT-1997;
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14-SEP-1998;
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21-NOV-1997;
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18-SEP-1997
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 The invention relates to sixty one nucleic acids encoding PRO
polypeptides (secreted and transmembrane). The polynucleotide is useful
in molecular biology, including uses as hybridisation probes, in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
chromosome and gene mapping, in generating acidine.
Creating a compinant techniques, and in generating PRO
polypeptides by recombinant techniques, and in generating either
development and screening of therapeutically useful reagents. The PRO
polypeptide or the antibody is used in preparing a medicament for
treating a condition responsive to the polypeptide or antibody, such as
mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
e.g. Alzheimer's disease and Parkinson's disease. Usher syndrome,
carrophia areata, angiogenesis, inflammatory disease e.g asthma and
rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
present sequence represents the amino acid sequence of a PRO polypeptide
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                                                                                                                                             Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Goddwski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Ather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%; Score 42; DB 6; Length 696; 63.6%; Pred. No. 67; 1. No. 67; 1. No. 67; 1. No. 67; No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted / transmembrane polypeptide PRO266.
                                                                                                                                                                                                                           Example 14; Fig 34; 481pp; English.
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970S-0059117P.
970S-0059117P.
970S-0059121P.
970S-0059122P.
970S-0059184P.
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                                                                                               WPI; 2003-331485/31.
                                                                                                                N-PSDB; ACA05412.
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17-SEP-1997;
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ABU67022 standard; protein; 696 AA.

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The invention relates to an isolated, secreted and transmembrane prolypeptide; termed PRO polypeptide. The polypeptide is useful for identifying agonists or antagonists of the polypeptide, for preparing confidentifying agonists or antagonists of the polypeptide, for preparing confidentifying agonists or antagonists of the polypeptide is also useful for recombinantly expressing those markers. The polypeptide is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The mucleic acid is useful as therapeutic confident in the preparation of PRO polypeptide, for antisense RNA and DNA, in the preparation of PRO polypeptide, for antisense RNA and DNA, in the preparation of PRO polypeptide, for cuseful in the development and screening of therapeutically useful construct hybridisation probes for mapping the gene which construct hybridisation probes for mapping the gene which cancer therapeutically useful in the development and screening of therapeutically useful cancer, and for generating probes for polymerase chain reaction (PCR), Northern analysis, Southern analysis of individuals with generic disorders, and for generating probes for polymerase chain reaction (PCR), Northern analysis, Southern analysis and Mestern analysis, of specific cells, tissues or serum and for affinity purification of PRO for antibody is useful for the preparation of medicament for treating obsesity, diabetes or antibody is useful for the preparation of medicament for treating obsesity, for inhibiting tumour growth, enhances vascular permeability and immune treating the angles or serum and for treating obsesity, diabetes or response, for inhibiting tumour growth, enhances vascular permeability and immune treating the aning loss in mammals and for treating bone and/or cartiage creating enemanders sequence of a human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                   Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski DJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005941.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US00439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
24-JUL-2000; 2000WO-US02710.
24-AUG-2000; 2000WO-US02328.
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N-PSDB; ACD20079.
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    56.8%; Score 42; DB 6; Length 696; 63.6%; Pred. No. 67; or Indels ive 4; Mismatches 0; Indels
Query Match
Best Local Similarity 63.6%;
Marches 7; Conservative
                                                               4 GMALSKINLHN 14
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|::|||::||| 493 GVSLSKLSLHN 503

RESULT 33 ABU67022

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Human, secreted protein, transmembrane protein, PRO; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birch defects; premature aging, AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tumour.
                                           Human secreted/transmembrane, PRO, protein SEQ ID 354.
                                                                                                                                                                                                                                                                                  99WO-US000106
99WO-US000109
99WO-US000150
99WO-US000615
99WO-US001073
99WO-US020111
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99WO-US02011090
99WO-US0201547
99WO-US021080
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99WO-US028551
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15-SEP-1999;
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24-FEB-2000;
01-MAR-2000;
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                            27-MAY-2003
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2001US-00860216.
2001US-00866028.
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Æ, Goddard
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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Stewart TA,
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N-PSDB; ACA04200.
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20-DEC-2000;
20-DEC-2000;
28-PEB-2001;
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05-APR-2001;
10-MAY-2001;
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14-MAR-2001;
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01-JUN-2001;
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28-JUL-2000;
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08-NOV-2000;
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                                                                                                                                                                                                                                                                                                           Baker KP,
                                                                                                                                                                                                                                                                                                                 Gerritsen
Smith V,
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Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 12; Fig 354; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DRA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO

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cc extracellular domains and mature sequences, methods of detecting PRO
crecrosis, methods for stimulating the release of TNF-alpha (tumour
cc differentiation of chondrocyte cells, the proliferation of
cartilage, proliferation of inner ear urticular supporting cells, the
cartilage, proliferation of inner ear urticular supporting cells, the
cartilage, proliferation of inner ear urticular supporting cells, the
cartilage, proliferation of inner ear urticular supporting cells, the
cproliferation of T-lymphocyte cells, the release of a cytokine from
cc proliferation of T-lymphocyte cells, the release of a cytokine from
c proliferation of T-lymphocyte cells, the release of a cytokine from
cc party acid (FPA) by skeletal muscle cells, a method for inhibiting the
cc fatty acid (FPA) by skeletal muscle cells, a method for inhibiting the
cc oligonucleotide probe derived from any of the nucleotide sequences cited
above. The nucleic acids and polypeptides are useful for treating
cc inflammatory diseases, organ failure, antheroseleroals, cardiac injury,
cinflammatory diseases, premature aging, AIDS (acquired
immunodeficiency syndrome), cancer, or diabetic complications. The
cmapping, and in generating antisenes RNA or DNA. The polypeptides are
cuseful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; gene therapy; psoriasis; enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation poithelial cancer; Alzheimer's disease; squamous cell carcinoma; parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cardiac injury; diabetic complication; wound repair; tissue re-growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU69637 standard; protein; 696 AA
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970S-0059124P.
970S-0059184P.
970S-0059263P.
970S-0059266P.
970S-0062285P.
970S-0062285P.
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97US-0059115P.
97US-0059117P.
97US-0059119P.
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493 GVSLSKLSLHN 503
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protein of the invention
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15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
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17-SEP-1997;
17-SEP-1997;
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97US-0063486P.
97US-0062814P.
97US-0063814P.
97US-0063121P.
97US-0063134P.
97US-0063138P.
97US-0063134P.
97US-006314P.
97US-006314P.
97US-006314A.
97US-006314A.
98US-01030194P.
98US-01030194P.
98US-01030194P.
98US-01030194P.
98US-0143048P.
99US-0145048P.
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2000WO-US003565.
2000WO-US004414.
2000WO-US005041.
2000WO-US005841.
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
25-OCT-1997;
28-OCT-1997;
28-OCT-1999;
28-OCT-1999;
38-OCT-1999;
38-OC
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The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal curers or useful in diagnosing or treating enterocolitis, gastrointestinal are useful in diagnosing or treating enterocolitis, gastrointestinal curers or ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoritasis or epithelial cancers such as equamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic atteral sclerosis, inflammatory disease, Parkinson's disease, amyotrophic asther or multiple sclerosis, premature aging, AIDS, cancer, injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are growth of tissue. The PRO polypeptides and nucleic acid molecules are calso useful in gene therapy, and as molecular weight markers for protein clectrophoresis purposes. The anti-PRO antibodies may be used in clectrophoresis proposed for PRO, or for the affinity purification of PRO from clecombinant cell culture or natural sources. This is the amino acid correction acid molecular maine acid molecular 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
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                                                                                                                                                                                                                                                           Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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30-MAR-2000; 2000MO-US008439.
22-MAY-2000; 2000MO-US014042.
02-UJN-2000; 2000MO-US012544.
28-UJL-2000; 2000MO-US020710.
24-AUG-2000; 2000MO-US023328.
18-SEP-2000; 2000US-00665350.
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N-PSDB; ACA54882.
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disease.
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9705-0052814P-
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99US-0145698P
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                US2003027143-A1.
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24-0CT-1997;
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29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
Homo sapiens.
                                                   16-JUL-2001;
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18.SEP-1997;
18.SEP-1997;
18.SEP-1997;
17.OCT-1997;
24.OCT-1997;
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24-NOV-1
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2000WO-US005841. 2000WO-US007377. 2000WO-US008439. 2000WO-US014042. 99WO-US021090. 99WO-US021547. 99WO-US021547. 99WO-US023089. 99WO-US028565. 99WO-US030095. 99WO-US030911. 2000WO-US003565. 2000WO-US004414. 2000WO-US005004. 2000WO-US015264. 2000WO-US020710. 2000WO-US023328. 99WO-US028214 99WO-US028313 2000WO-US000219 2000US-00665350 99WO-US028301 99WO-US028564 01-DEC-1999; 02-DEC-1999; 02-DEC-1999; 16-DEC-1999; 20-DEC-1999; 24-FEB-2000; 02-MAR-2000; 11-FEB-2000; 22-FEB-2000; 20-MAR-2000; 30-MAR-2000; 13-SEP-1999; 15-SEP-1999; 15-SEP-1999; 22-MAY-2000; 02-JUN-2000; 05-JAN-2000; 05-OCT-1999 29-NOV-1999 NOV-1999

(GETH) GENENTECH INC.

Ä Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard J Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D; Wood WI; Godowski PJ, Grima Mather JP, Pan J, Williams PM, Ashkenazi A, Filvaroff E,

WPI; 2003-417249/39. N-PSDB; ACD19717.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.

Claim 12; Fig 34; 467pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptides are useful for modulating biological activity of a cell, in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for in gynaecological diseases e.g. to avoid or lessen the need for condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lessons, skin diseases associated with abnormal keratinocyte (asteroristical of e.g. psoriasis), Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies, disease cascade disorders, neurodegenerative disease, thrombosis, hamorrhage, cascade disorders, neurodegenerative disease, thrombosis, hamorrhage, candometrial bleeding, wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and in the generating transgenic animals or knockout animals. The PRO cappeptides and their nucleic acids are useful for tissue typing. PRO cappeptides and their nucleic acids are useful for tissue typing. PRO cappeptides and their nucleic acids are useful for tissue typing. PRO campibodies are useful for dispussion in specific cells, tissue typing. PRO cappides and their PRO antibodies are useful in diagnostic assays for sources. The present sequence represents the amino acid sequence of a human secreted and transmembrane PRO polypeptide

Sequence 696 AA;

6; Length 696; Score 42; DB Pred. No. 67; 56.8%; Query Match Best Local Similarity

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Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
Human; secreted and transmembrane protein, PRO;
Tumour necrosis factor alpha release; TNR-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
lung tumous; colon tumour; Dreast tumour; prostate tumour; rectal tumour; cervical tumour; cervical tumour; cervical tumour; cervical tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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98WO-US014556.
98WO-US014818.
98WO-US017818.
98WO-US0118124.
98WO-US011817.
98WO-US012131.
98WO-US02292.
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98WO-US02292.
99WO-US02615.
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99WO-US028551.
99WO-US028564.
99WO-US028565.
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99WO-US030999.
99WO-US030720.
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GVSLSKLSLHN 503
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12-JUN-1998;

14-JUN-1998;

14-SEP-1998;

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16-SEP-1998;

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10-MAR-1999;

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30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031244.
50-JAN-2000; 2000WO-US000219.
66-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US000371.
12-FEB-2000; 2000WO-US000341.
13-FEB-2000; 2000WO-US0004142.
22-FEB-2000; 2000WO-US0004142.
24-FEB-2000; 2000WO-US0004142.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US000414.
24-FEB-2000; 2000WO-US00546.
11-MAR-2000; 2000WO-US005419.
25-MAR-2000; 2000WO-US005419.
20-MAR-2000; 2000WO-US00737.
21-MAR-2000; 2000WO-US00737.
21-MAR-2000; 2000WO-US00737.
21-MAR-2000; 2000WO-US00737.
21-MAR-2000; 2000WO-US00737.
22-MAR-2000; 2000WO-US00737.
23-MAR-2000; 2000WO-US017404.
23-MAR-2001; 2000WO-US01749.
24-MAR-2001; 2000WO-US01749.
25-MAR-2001; 2000WO-US01749.
25-MAR-2001; 2001WS-0088619.
25-MAR-2001; 2001WS-0088619.
25-MAR-2001; 2001WS-0088619.
25-MAR-2001; 2001WS-0088619.
25-MAR-2001; 2001WS-00887876.
25-MAR-2001; 2001WS-008878776.
25-MAR-2001; 2001WS-00887876.
25-MAR-2001; 2001WS-00887876.
25-MAR-2001; 2001WS-008878776.
25-MAR-200
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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N-PSDB; ADA45872.
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20-DBC-2000; 2000US-00747259.
20-DBC-2000; 2000W0-US034956.
28-FEB-2001; 2001US-0079620.
28-FEB-2001; 2001W0-US006520.
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14-SEP-1998;
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22-FEB-2000;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the crelease of TWF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in perioryte cells, for stimulating the proliferation of or gene expression in perioryte cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of finer ear utricular supporting cells, for stimulating the proliferation of finer ear utricular supporting cells, cor stimulating the proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, correlations prolating genomic and cDNA nucleotide sequences or actisens probes. (I) is also useful st herapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in terraction. A polymucleotide (II) encoding (I) is useful in chromosome cor and gene mapphing, in generating transgenic animals or knockout animals which in turn are useful in the development and corposes. An anti-(I)-antibody is useful in diagnostic assays for PRO, error corposes. An anti-(I)-antibody is useful in diagnostic assays for PRO, encombinant cell culture or natural colling its expression in specific cells, itsense or serum, and for sources. (I) and (II) are useful for tissue typing. This is the amino colling the useful for tissue typing. This is the amino colling the movel human secreted and transmembrane PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA76304 standard; protein; 696 AA.
                      Claim 12; Fig 354; 659pp; English
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Best Local Similarity 63.6
Matches 7; Conservative
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ADA76304
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypuclocides encoding them. The invention also relates to an antibody which specifically binds to a PRO cinvention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as a tips and in gene therapy. The polymucleotides may also artisense RNA and DNA and in gene therapy. The polymucleotides may also contisense the prostating atther transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful useful in the development, for scinniarial and input to the polypeptides or medicament for transfing a condition responsive to the polypeptides or medicament for transfing a condition responsive to the polypeptides or stimulating the upcake of continuating differential muscle cells, for adipocyte cells, for stimulating the proliferation of orgene expression in periotyce cells, for transfing the proliferation of inner ear usticular supporting cells or T-lymphocyte cells, for inducing endotheblal cell tube formation and for transfing the proliferation of inner ear usticular supporting cells or transing continuations become and/or cartilage defects, osteoarthritis and rheumatoid arthritis. Row polypeptides which stimulate the release of proteoglycans from artilage are useful for treating sports release of proteoglycans articular cartilage defects, osteoarthritis and rheumatoid arthritis. The inventeer such as various thalassaemias and conditions which may benefit from enhanced 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-MAR-2001; 2001WO-US00666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00802706.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-008167428.
10-MAY-2001; 2001US-00854280.
10-MAY-2001; 2001US-00854280.
11-MAY-2001; 2001US-00866018.
25-MAY-2001; 2001US-00866018.
25-MAY-2001; 2001US-00866018.
25-MAY-2001; 2001US-00866018.
25-MAY-2001; 2001US-00866018.
25-MAY-2001; 2001US-0086618.
25-MAY-2001; 2001US-0086618.
25-MAY-2001; 2001US-0086618.
25-MAY-2001; 2001US-0088769.
20-JUN-2001; 2001US-0088769.
20-JUN-2001; 2001US-00887879.
20-JUN-2001; 2001US-00987879.
18-JUN-2001; 2001US-00924419.
19-DEC-2001; 2001US-00931836.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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N-PSDB; ADA76303.
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Human, PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
sequence data for this patent is also available in electronic format from
USPTO at seqdata.uspto.gov/sequence.html.
                                                                          Gaps
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                                                    Length 696;
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                                                    Score 42; DB 6; Pred. No. 67; 4; Mismatches
                                                                                                                                                                                                                                     Human secreted/transmembrane protein, #18.
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97US-0059113P
97US-0059117P
97US-0059121P
97US-0059124P
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97US-0059184P
97US-0062185P
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97US-006214P
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                                             493 GVSLSKLSLHN 503
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                                  Sequence 696 AA;
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Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal
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Gerritsen
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W, Gerber H,
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Paoni NF, Roy MA,
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Grimaldi JC, Gu
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9705-0066840P.
9705-0069425P.
9805-009803P.
9805-009803P.
9805-0100262P.
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99US-0146222P.
99WO-US020594.
                    97US-0063870P.
97US-0064103P.
97US-0064248P.
97US-0064809P.
97US-0065846P.
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97US-0066364P.
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97US-0066511P.
97US-0066770P.
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98US-0100858P.
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Fong S, Gac
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Williams PM,
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Filvaroff E,
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03-NOV-1997;
07-NOV-1997;
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               29-OCT-1997
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                                                                                           NOV-1
                                                                                                                                                                                                      17-SEP-1
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The invention discloses isolated PRO secreted/transmembrane polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that gecifically bind to the PRO polypeptide for linking a tamibodies that gecifically bind to the PRO polypeptides are useful for adaltating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a talest one biological activity of a cell. PRO polypeptides are also useful for detecting discorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal leions, skin diseases associated with the proservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal leions, skin diseases associated with the proservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal leions, skin diseases related to uncontrolled cell growth, e.g. cancer. Additionally disease related to uncontrolled cell growth, e.g. cancer. Additionally disease related to uncontrolled cell growth, e.g. cancer. Additionally disease related to uncontrolled cell growth, e.g. cancer. Additionally in requesting other pro-sesociated disorders, in modulating chromic agent with reduced risk for heamorrhage as compared with network as role in neurodegenerative diseases or their reversal, as an arithrombotic agent with reduced risk for heamorrhage as compared with have a role in apoptosis, the polymucleotides are useful in chromosome and gene mapping in the generation of antisense RNA and DNA, consome and gene mapping in the generation of antisense RNA and DNA chromosome and gene mapping in the development and screening of individuals which are useful in the development and screening of the respective secondarial as molecular marker for process electrication of control cells, tissues or serum and for affinity purification of the PRO polypeptide (agnited) or prevent the ef ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher Gaps ö 6; Length 696; 0; Indels Score 42; DB 6 Pred. No. 67; 4; Mismatches ADA18954 standard; protein; 696 AA. Claim 12; Fig 34; 469pp; English 56.8%; Human PRO polypeptide #177. (first entry) Local Similarity 63.6 493 GVSLSKLSLHN 503 4 GMALSKINLHN 14 Sequence 696 AA; 20-NOV-2003 ADA18954; Query Match Best Loc Matches RESULT 39 ADA18954 ò 셤 *******

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;

Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D;

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colon; breast; prostate; rectum; cervix; liver; tumour; cancer; glucose uptake; FFA, adipocyte cell; pericyte cell; proteoglycan; cartilage; inner ear utricular supporting cell; cytokine; A-peptide; factor VIIA; endothelial cell.
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                                                                            Homo sapiens
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
30-MAY-2000; 2000MO-US014941.

02-JUN-2000; 2000MO-US015264.
28-JUL-2000; 2000MO-US015252.
24-AUG-2000; 2000MO-US023328.
08-NOY-2000; 2000MO-US023328.
08-NOY-2000; 2000MO-US023328.
01-DEC-2000; 2000MO-US033678.
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01-DEC-2000; 2000MO-US033678.
01-DEC-2000; 2000MO-US034956.
01-MAR-2001; 2001US-00086520.
01-MAR-2001; 2001US-00866520.
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01-MAR-2001; 2001US-00866520.
01-MAR-2001; 2001US-0086669.
01-MAR-2001; 2001US-00866216.
01-MAY-2001; 2001US-00866216.
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01-JUN-2001; 2001US-0086431.
01-JUN-2001; 2001US-0086436.
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N-PSDB; ADA18953.
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3 Gao

New PRO nucleic acid, useful for preparing a composition for treating e.g., tumors.

Claim 12; Fig 354; 660pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. lung, colon, breast, profileration or differentiation of chondrocyte cells and a method for testing the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in Chromosome and gene mapping, in generating antisense RNA and DNA and in Chromosome and gene mapping, in generating antisense RNA and bNA and in Chromosome and gene mapping, in cluding uses as hybridisation PRO colophypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the colophypeptides or antibodies are used in preparing a medicament for trating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for trating a condition responsive to the polypeptides or antibodies are used in preparing a such as tumours, for modulating the uptake of glucose or FRA by adipocyte cells, for stimulating the release of proteoglycans from

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99WO-US020111.
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                                                                                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the release of cytckines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells and for stimulating the proliferation of endothelial cells. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the control of the invention of the invention of the cells, for release of TNP-labha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or dispocyte cells, for stimulating the proliferation of fore expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of T-lymphocyte cells, for stimulating of the presence of unmour in a mammal. The tumour is lung, colon, breast, cells, for stimulating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent, proliferation of antisense probes. (1) is also useful as therapeutic agent, in the inner provided in binding interaction A polyuncleotide (11) encoding (1) is useful in chromosome content of PRO polypeptide, for generating transgents and profice cells, in generation of antisense RNA and bNA, in the concent of an open content and secreting of therapeutically useful reagents, in generation of secreting its expression in specific cells, tissues or serum, and for cereating the sexpression in specific cells, tissues or serum, and for concent.) and sequence of a novel human secreted and transmembrane PRO
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                                                                                                                                                                                                     Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                               New PRO nucleic acid and encode polypeptides, are useful for manufacturing a medicament for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 354; 660pp; English.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00931836.
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N-PSDB; ADA61576.
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Match 56.8%; Score 42; DB 6; Length 696; Local Similarity 63.6%; Pred. No. 67; ce 7; Conservative 4; Mismatches 0; Indels 4 GMALSKINLHN 14 Query Match Best Local S: Matches 7

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 357739, Application US/10425115

Publication No. US20040214272A1

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Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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US-10-425-115-367739
PRIOR APPLICATION NUMBER: US 60/444,113
PRIOR FILING DAFE: 2003-01-31
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 8; Conservative
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ORGANISM: M. catarrhalis
US-10-769-514-16
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US-10-769-514-15
Sequence 15, Application US/10769514
Sequence 15, Application US/10769514
Sequence 15, Application No. US20040258695A1
GENERAL INFORMATION NO. US20040258695A1
TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
FILE REFERENCE: 028722-011
CURRENT PELLON NUMBER: US/10/769,514
CURRENT PILLING DATE: 2003-01-30
PRIOR PILLING DATE: 2003-01-30
PRIOR PILLING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                      Sequence 17, Application US/10769514

Publication No. US20040258695A1

Publication No. US20040258695A1

Publication No. US20040258695A1

APPLICANT: Schryvers, Anthony

TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof

FILE REFERENCE: 029722-001

CURRENT APPLICATION NUMBER: US/10/769,514

CURRENT PILING DATE: 2003-01-30

PRIOR FILING DATE: 2003-01-31

PRIOR FILING DATE: 2003-01-31

NUMBER OF SEQ ID NOS: 86

SOFTWARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 14; Conservative 0; Mismatches
                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: M. catarrhalis
US-10-769-514-17
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US-10-769-514-15
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MS-10-424-599-250435

| Sequence 250435, Application US/10424599
| Sequence 250435, Application US/10424599
| Sequence 250435, Application No. US20040031072A1
| GENERAL INFORMATION:
| Publication No. US2004003107A1
| GENERAL INFORMATION:
| APPLICANT: La Kovalic David K
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants: US/10/424,599
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 285684
| SEQ ID NO 250435
| LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_68170C.1.pep
US-10-424-599-250435
2 GYGMALSKINL 12
                                    17 GYGYSISKINL 27
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ORGANISM: Glycine max
FEATURE:
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1 MGYGMALSKINLHN 14

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Score 44; DB 4; Length 64; Pred. No. 3.6; 2; Mismatches 1; Indels

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APPLICANT: Avans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Grack, Hilary
APPLICANT: Grack, Hilary
APPLICANT: Grackiel, Kim
APPLICANT: Genetics Institute, Inc.
TILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TILE OF INVENTION: SECRETED PROTEINS AND FOLYNUCLEOTIDES ENCODING THEM
TILE REFERRENCE: 00766.00103.5
CURRENT APPLICATION NUMBER: US/10/616,263
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
SOFTWARE PATENTING VET. 2.00
SEQ ID NO 132
LENGTW-
Gaps
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Pred. No. 1.1e+02;
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  Mismatches
                                                                                                                                                                           ; Sequence 132, Application US/10616263; Publication No. US20040038276A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 91, Application US/09909320 Patent No. US2002013240A1 GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
    4;
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Filvaroff, Ellen
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Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kljavin, Ivar J.
Mather, Jennie P.
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Botstein, David
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Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
Eaton, Dan L.
  7; Conservative
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492 GVSLSKLSLHN 502
                                                                                                                                                                                                                                            APPLICANT: Jacobs, Kenneth
                                                                |::|||::|||
492 GVSLSKLSLHN 502
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                                         4 GMALSKINLHN 14
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CORGANISM: Homo sapiens
US-10-616-263-132
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                                                                                                                                                              US-10-616-263-132
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US-09-909-320-91
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APPLICANT:
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APPLICANT
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      Matches
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                                                                                                                                                                                                                         Sequence 19, Application US/10424233

Sequence 19, Application US/10424233

Bublication No. US20030220263A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: EXPRESSED IN THE NERVOUS SYSTEM
FILE REPERENCE: D0233 NP
CURRENT APPLICATION NUMBER: US/10/424,233
CURRENT FILING DATE: 2003-04-25
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 19
LENGTH: 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y sequence 112, Application US/09374046A

y Bedlication No. US20030096951A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: LaVallie, Edward R.

APPLICANT: LaVallie, Edward R.

APPLICANT: LaVallie, Edward R.

APPLICANT: Brans, Cheryl

APPLICANT: Brans, Cheryl

APPLICANT: Stalinger II, Robert J.

APPLICANT: Spaliding II, Robert J.

APPLICANT: Spaliding Vikki

APPLICANT: Stalinger II, Robert J.

APPLICANT: Grack, Hilary

APPLICANT: Glark, Hilary

APPLICANT: Glark SECKETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

TUTLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES

CURRENT FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 132

LENTHE BREENERING SECRETED PROTEINS AND POLYNUCLEOTIDES

LENTH: 695

LENTH: 695

LENTH: 695
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98;
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                           DB 4; Length 71;
                                                              4; Indels
                                                                3; Mismatches
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Pred. No. 9
                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.8%;
                           Query Match 58.1%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                        1 MGYGMALSKINLHN 14
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58 LGYGLTYDKENLHD 71
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Best Local Similarity 63.6
Matches 7; Conservative
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432 GVSLSKLSLHN 442
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; ORGANISM: Homo sapiens
US-10-424-233-19
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Best Local Similarity
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Gaps

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APELICANI: Grimaldi, Christopher J.
APELICANI: Grimaldi, Christopher J.
APELICANI: Gurney, Austin L.
APELICANI: Gurney, Austin L.
APELICANI: Klavia, Yaux J.
APELICANI: Klavia, Yaux J.
APELICANI: Klavia, Yaux J.
APELICANI: Klavia, Yaux J.
APELICANI: Rabi, Jame P.
APELICANI: Pan, Jame P.
APELICANI: Pan, Jame P.
APELICANI: Pool, Wicholas F.
APELICANI: Roy, Magaret Ann
APELICANI: Roy, Magaret Ann
APELICANI: Roy, Magaret Ann
APELICANI: Mood William, P.
APELICANI: Wood William, P.
APELICANION WORBER: US/09/2034
BRIOR APELICANION WORBER: US/09/2034
BRIOR APELICANION WORBER: CPT/US99/2139
BRIOR APELICANION WORBER: CPT/US99/2139
BRIOR APELICANION WORBER: PCT/US99/2139
BRIOR APELICANION WORBER: PCT/US99/21399
BRIOR PLING DATE: 11299-112-126
BRIOR APELICANION WORBER: PCT/US99/21399
BRIOR PLING DATE: 11299-112-126
BRIOR APELICANION WORBER: PCT/US99/21399
BRIOR PLING DATE: 11200-1120
BRIOR PLING DATE: 11200-1120
BRIOR APELICANION WORBER: PCT/US99/21399
BRIOR PLING DATE: 11200-1120
BRIOR APELICANION WORBER: PCT/US99/213999
BRIOR PLING DATE: 11200-1120
BRIOR PLING DATE: 11200-11200
BR
                                                                                                              Godowski, Paul J.
Grimaldi, Christopher J.
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
        APPLICANT: Stewart, Timotny A.

APPLICANT: Williams, Dania, B.

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: MUMBER: US/09/909,320

CURRENT FILING DATE: 2000-20.20

PRIOR PLILNG DATE: 1299-70-70

PRIOR PLILNG DATE: 1299-70-70

PRIOR PLILNG DATE: 1399-70-70

PRIOR PLILNG DATE: 1399-70-70-80-18

PRIOR PLILNG DATE: 1399-70-70-80-18

PRIOR PLILNG DATE: 1399-70-10-13

PRIOR PLILNG DATE: 1399-70-10-13

PRIOR PLILNG DATE: 1399-10-15

PRIOR PLILNG DATE: 1399-11-00-15

PRIOR PLILNG DATE: 1399-11-00-15

PRIOR PLILNG DATE: 1399-11-00-15

PRIOR PLILNG DATE: 1399-10-15

PRIOR PLILNG DATE: 1399-10-15

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    Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-91
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                                                                                                       Gaps
                                                                                                       0
                                                                   Length 696;
                                                                   Query Match 56.8%; Score 42; DB 3; Length 696
Best Local Similarity 63.6%; Pred. No. 1.1e+05.
Matches 7; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                   |::|||::|||
493 GVSLSKLSLHN 503
                                                                                                                                           4 GMALSKINLHN 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-91
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RESULT 10
US-09-909-088B-91
Sequence 91, Application US/0990908B
Sequence 91, Application US/0990908B
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi.
APPLICANT: Becterin, David
APPLICANT: Becon, Dan L.
APPLICANT: Ferrara Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
POPLICANT: Fong, Sherman
POPLICANT: Gao, Wei-Qiang

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RESULT 11 US-09-905-291A-91

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Query Match
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIO
Sequence 91, Application US/09905291A
Patent No. US20020150374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-905-291A-91
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APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT APPLICATION NUMBER: US/09/665,350
RIGH APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21091
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-26
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     Length 696;
Score 42; DB 3; Length 696
Pred. No. 1.1e+02;
4; Mismatches 0; Indels
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Grimaldi, Christopher J.
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  56.8%;
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Hillan, Kenneth, J.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                              Best Local Similarity 63.0
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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US-09-902-853-91
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APPLICANT:
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APPLICANT:
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APPLICATION NUMBER: PCT/US99/21547
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APPLICANT: Gac, Wei-Janag
APPLICANT: Garber, Hangbear
APPLICANT: Gac, Wei-Janag
APPLICANT: Gacher, Hangbear
APPLICANT: Gacheri, Paul J.
APPLICANT: Gacheri, Paul J.
APPLICANT: Gacheri, Paul J.
APPLICANT: Garmaldi, Christopher J.
APPLICANT: Gurmer, Austin L.
APPLICANT: Gurmer, Austin L.
APPLICANT: Gurmer, Jennie P.
APPLICANT: Hallan, Kenneth, J.
APPLICANT: Paul Janes
APPLICANT: William, P. Mickey
APPLICANT: Wood, WOOG, WILLIAM, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION NUMBER: US/09/907,824
CURRENT APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
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| PRIOR APPLICATION NUMBER: PCT/US99/30911 |
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR PLILING DATE: 1999-12-20 |
| PRIOR APPLICATION NUMBER: PCT/US99/3099 |
| PRIOR PELLING DATE: 1999-12-20 |
| PRIOR PLILING DATE: 1999-12-20 |
| PRIOR FILING DATE: 2000-01-05 |
| NUMBER OF SEQ ID NOS: 423 |
| LENGTH: 696 |
| TYPE: PR |
| TYPE: PR |
| TYPE: PR |
| GRAMISM: Homo Sapien |
| US-09-902-853-91
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Beton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timochy A.
APPLICANT: Thums, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Best Local Similarity 63.6%; Pred. No. 1.14+02.
Matches 7; Conservative 4; Mismatches 0; Indels
Matches 7; Conservative 4; Mismatches 0; Indels
PRIOR FILING DATE: 1999-125

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR APPLICATION NUMBER: PCT/US99/28131

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PLING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 2000-01-05

NUMBER: PCT/US00/00219

PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 696
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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US-09-907-841-91
; Sequence 91, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Garber, Hanspeter
Gerriteen, Mary E.
Goddard, A.
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US-09-907-824-91
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US-09-903-640-91
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/USO0/0414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLILNG DATE: 1999-07-26
PRIOR PLILNG DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PLILNG DATE: 1999-09-09
PRIOR PLILNG DATE: 1999-09-09
PRIOR PLILNG DATE: 1999-09-13
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PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
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PRIOR PLING DATE: 1999-11-29
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Pred. No. 1.18+02;
i; Mismatches 0; Indels
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Publication No. US20030003530A1
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 63.6
Matches 7; Conservative
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Eaton, Dan L.
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493 GVSLSKLSLHN 503
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CRGANISM: Homo sapiens
US-09-907-841-91
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LENGTH: 696
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Pred. No. 1.1e+02;
4; Mismatches 0
                                                                PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PRILICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
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PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Bilen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Geritsen, Mary E.
Goddard, A.
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Mather, Jennie P
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 63.6
Matches 7; Conservative
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Eaton, Dan L.
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493 GVSLSKLSLHN 503
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US-09-904-011-91
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PRIOR PELICATION NUMBER: PCT/US99/20948
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-06
PRIOR PELICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28656
PRIOR PELICATION NUMBER: PCT/US99/3099
PRIOR PELING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William, I.
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ilvaroff, Ellen
ong, Sherman
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
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US-09-906-742-91
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Aucholas F.

Acoy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Acids Encoding the Same

FILE REPRENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/903,640

CURRENT APPLICATION NUMBER: 09/655,350

PRIOR FILING DATE: 2001-07-11

PRIOR FILING DATE: 2001-07-11

PRIOR FILING DATE: 2000-09-18

NUMBER OF EQ. ID NOS: 423

LENGTH: 696
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paul, James P.
APPLICANT: Paul, James P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Trans, Daniel P.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE APPLICATION NUMBER: US/09/908,093
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2000-032-22
PRIOR PILING DATE: 1099-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLICATION NUMBER: US 60/145,698
PRIOR PAPLICATION NUMBER: US 60/146,222
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; Sequence 31, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerriteen, Mary E.
Goddard, A.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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; ORGANISM: Homo Sapien
US-09-903-640-91
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Query Match 56.8%; Score 42; DB 3; Length 696; Best Local Similarity 63.6%; Pred. No. 1.1e+02; Matches 7; Conservative 4; Mismatches 0; Indels
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: 10466-14 Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 Secreted and Transmembrane Secreted 
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63.6%; Pred. No. 1.1e+02;
ive 4; Mismatches 0; Indels
                                                Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Best Local Similarity 63.6
Matches 7; Conservative
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US-09-906-838-91
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US-09-907-613-91
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ORGANISM:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBENE: 1046-61.

FILE REPERBENE: 1046-61.

CURRENT APPLICATION NUMBER: 09/66,742

PRIOR APPLICATION NUMBER: 09/66,742

PRIOR APPLICATION NUMBER: 09/61-61

PRIOR APPLICATION NUMBER: 06/143,048

PRIOR APPLICATION NUMBER: 06/145,698

PRIOR APPLICATION NUMBER: 06/146,222

PRIOR APPLICATION NUMBER: 06/146,222

PRIOR APPLICATION NUMBER: 06/146,222

PRIOR APPLICATION NUMBER: 06/146,222

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-25

PRIOR PILING DATE: 1999-10-25

PRIOR PILING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-39

PRIOR PELING DATE: 
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
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Publication No. US20030027143A1
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: ABhkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferzara, Napoleone
APPLICANT: Filvaroff, Ellen
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Homo Sapien
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I Goffild A. I.

M.T. Kljatuk, Ameth. J.

M.T. Kljatuk, Ivar J.

ANT: Mather Jennie P.

ANT: Rey, Margaret An.

CANT: Stevent: Timeth A.

ANT: Mach. Thumas, Daniel P.

ANT: Mach. Thumas, Daniel P.

ANT: Mach. Thumas, Daniel P.

CANT: Stevent: Timed A.

ICANT: Thumas, Daniel A.

ICANT: Wood, William P. Mickey

ICANT: Wood, William P. William P.

RENGR FILING DATE: 1999-10-10

PRIOR PARICATION WOOGHS: POT-1099/2014

PRIOR PALICATION WOOGHS: POT-1099/2014

PRIOR PALICATION WOOGHS: POT-1099/2016

PRIOR PALICATION WOOGHS: POT-1099/2019

PRIOR PALICATION WOOGHS: 
Sequence 91, Application US/09907613;
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botatein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
Goddard, A.
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Score 42; DB 3; Length 696;
Pred. No. 1.1e+02;
4; Mismatches 0; Indels
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US-09-907-942-91
; Sequence 91, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
   Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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PPLICANT: Stewart, and the state of the stat
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FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
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Publication No. US20030036061A1
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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493 GVSLSKLSLHN 503
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US-09-904-859-91
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 91
LENGTH: 696
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Publication No. US20030036060A1
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Pilvaroff, Ellen
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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493 GVSLSKLSLHN 503
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US-09-907-942-91
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US-09-904-859-91
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-00-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-04
PRIOR PLING DATE: 1999-12-04
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-1
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
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       Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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US-09-904-820-91
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US-09-904-786-91
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Go.8%; Score 42; DB 3; Length 696; Best Local Similarity 63.6%; Pred. No. 1.1e+02;

Matches 7; Conservative 4; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 1999-12-16
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SENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bankenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, Dan L.
APPLICANT: Ferrara, Napoleone
PLICANT: Fong, Sherman
UICANT: Fong, Sherman
UICANT: Gerber, Hanspeter
CANT: Gerber, Hanspeter
CANT: Gerber, Hanspeter
CANT: Godwari, Paul J.
NT: Ginney, Austin L.
Hillan, Kenneth, J.
Hillan, Kenneth, J.
Hillan, Kenneth, J.
Hillan, Kenneth, J.
Hather, Jennie
Pan, Jenne
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-204-91
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US-09-904-820-91
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US-09-906-100-91
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APPLICANT:
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APPLICANT:
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                   Ladn, Kenneth, J.

Liavin, Ivar J.

Kijavin, Ivar J.

Kijavin, Ivar J.

Kijavin, Ivar J.

Mather, Jennie P.

APPLICANT: Mather, Jennie P.

APPLICANT: Pani, James

APPLICANT: Pani, Micholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Timethy A.

APPLICANT: William, P. Mickey

APPLICANT: William, P. Mickey

APPLICANT: William, P. Mickey

APPLICANT: William, I.

TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 91

LENGTH: 696

TTPLE: PPT
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Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Gerritsen, Mary E.
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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::|||::|||
493 GVSLSKLSLHN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT

ORGANISM: Homo Sapien

US-09-904-786-91
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Gaps
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Pred. No. 1.1e+02;
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THILE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,646

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US/09/906,4414

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07
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Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.8%;
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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, ORGANISM: Homo sapiens
US-09-906-646-91
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Renneth, J.
APPLICANT: Hillan, Renneth, J.
APPLICANT: Hillan, Janes
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy R.
APPLICANT: Stewart, Timothy A.
APPLICANT: Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE DEFRENCE: 10466-14

CURRENT APPLICATION NUMBER: 05/05/350

PRIOR FILING DATE: 2001-07-11

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1000-02-2

PRIOR PILING DATE: 1000-02-2

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-12-00

PRIOR FILING DATE: 1999-12-00

PRIOR PILING DATE: 1999-10-00

PRIOR PILING DATE: 19
                                                                                                                                                                                                                                                                                                                                                                              Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
CANT: Gurney, Austin L.

COANT: Hillan, Kenneth. J.

COANT: Band, Mischlan F.

LICHAT: Walliams. P. Macker

TILLS DATE: Date: Date: J.

TILLS DATE: Date: J. Macker

TILLS DATE: Date: J. Macker

TILLS DATE: Margineth M. Millan. J.

THE OF TREATHER DATE: 2000-09-18

REIGH PELICATION NUMBER: DC/146,0414

REIGH RAPLICATION NUMBER: PC/1899/21040

REIGH REILLS DATE: 1999-09-12 00

REIGH REILLS DATE: 1999-09-12 00

REIGH REILLS DATE: 1999-10-12 00

REIGH REILLS DATE: 1999-11-20

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56.8%; Score 42; DB 3; Length 696;

Best Local Similarity 63.6%; Pred. No. 1.1e+02;

Matches 7; Conservative 4; Mismatches 0; Indels
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Score 42; DB 3; Length 696; Pred. No. 1.1e+02; 56.8%; TYPE: PRT , ORGANISM: Homo Sapien US-09-903-786-91 Query Match Best Local Similarity

RESULT 28
10S-09-903-786-91
Sequence 91, Application US/09903786
Publication No. US20030044793A1
GENERAL INFORMATION:
APPLICANT: Genencech, inc.
APPLICANT: Ashkenazi, Avi

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Gaps

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AFELICANT: WOOD, WILLIAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,749A
CURRENT FILING DATE: 2001-07-11
PRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
                                                                                                                                                                                                                                           Score 42; DB 3; Length 696; Pred. No. 1.1e+02; 4; Mismatches 0; Indels
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APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 91
LENGTH: 696
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APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 91, Application US/09903749A publication No. US20030045693A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 63.6
Matches 7; Conservative
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Eaton, Dan L.
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Gao, Wei-Qiang
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493 GVSLSKLSLHN 503
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                                                                                                                                                   TYPE: PRT
CAGANISM: Homo sapiens
US-09-902-903-91
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               Indels
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               4; Mismatches
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TTLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR PLICATION NUMBER: PCT/US99/2069-09
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30911
APLICATION NUMBER: PCT/US99/30999
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Grimaldi, Christopher J.
Gurney, Austin L.
                                                                                                                                                                                                                       Sequence 91, Application US/09902903
Publication No. US20030044839A1
GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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Gao, Wei-Qiang
                 7; Conservative
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493 GVSLSKLSLHN 503
                                                              4 GMALSKINLHN 14
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APPLICANT:
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PRIOR APPLICATION NUMBER: 0200-07-11
PRIOR APPLICATION NUMBER: 0200-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR APPLICATION WHERE: PCT/US00/04414
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER: PCT/US09/30999
PRIOR PLING DATE: 2000-01-05
NUMBER: PCT/US00/00219
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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US-09-904-119-91
Sequence 91, Application US/09904119
; Publication No. US20030049621A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botatein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Beron, Dan L.
APPLICANT: Ferrara, Napoleone
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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| PRIOR PELING NATE: 1992-07-26
| PRIOR PELING NATE: 1992-07-28
| PRIOR PELING NATE: 1992-09-06
| PRIOR PELING NATE: 1992-09-016
| PRIOR PELING NATE: 1992-09-15
| PRIOR PELING NATE: 1993-09-15
| PRIOR PELING NATE: 1993-09-16
| PRIOR PELING NATE: 2000-10-16
| PRIOR PELING NATE: 2000-10-16
| PRIOR PELING NATE: 2000-10-16
| PRIOR PELING NATE: 3000-10-16
| PRIOR PELING NATE: 3000-10-
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APPLICANT: Thuse, Daniel
APPLICANT: Thuse, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wolliams, Daniel
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-41
FILE REFERENCE: 10466-41
FILE REFERENCE: 10466-41
FRICH APPLICATION NUMBER: 09/66,350
FRIOR FILING DATE: 2000-09-10
FRIOR FILING DATE: 2000-09-10
FRIOR PELING NUMBER: 09/66,350
FRIOR PELING NUMBER: 00-00-22
FRIOR APPLICATION NUMBER: 06/14,68
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-09-16
FRIOR PELING DATE: 1999-10-16
FRIOR PELING DATE: 1999-11-06
FRIOR PELING DATE: 1999-11-06
FRIOR PELING DATE: 1999-12-06
FRIOR PELIN
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
                                Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Best Local Similarity 63.6
Matches 7; Conservative
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US-09-902-736-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-09-907-794-91
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OP INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OP INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 10461-11 
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Pred. No. 1.18+02;
4; Mismatches 0; Indels
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Best Local Similarity 63.6%;
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-09-907-794-91
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T. Goddard, A., M.
T. Goddard, A., M.
T. Goddard, A., M.
T. Goddard, A., M.
T. Grandlai, thristopher J.
NT. Grandlai, thristopher J.
NT. Grandlai, thristopher J.
NT. Hillan, Romneth, J.
NT. Hillan, Romneth, J.
NATT. Bahber, Johnin, Tokar J.
LONTI. Brown Mallami, P. McKey
LONTIN, Thumas, Daniel
LON
Sequence 91, Application US/09907794 Publication No. US20030049677A1 GENERAL INFORMATION:
                                                                 T: Genericot, Inc.
T: Ashkenazi, Avi
Betsetein, David
Desnoyers Luc
Ferrara, Napoleone
Flivaroff, Blen
Fong, Sherman
Gao, Wei-Olang
Gerber, Hanspeter
Gertitsen, Mary E.
Goddard, A.
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Query Match 56.8%; Score 42; DB 3; Length 696; Best Local Similarity 63.6%; Pred. No. 1.1e+02; Matches 7; Conservative 4; Mismatches 0; Indels
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Publication No. US20030054349A1
GENERAL INFORMATION:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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                                                                              PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Desnoyers, Luc
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Best Local Similarity 63.6
Best Toons 7; Conservative
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493 GVSLSKLSLHN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eaton, Dan L.
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, ORGANISM: Homo Sapien
US-09-904-462-91
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APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US99/28000.
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 91
LENGTH: 696
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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493 GVSLSKLSLHN 503
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CORGANISM: Homo Sapien
US-09-903-943-91
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US-09-904-462-91
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US-09-903-520-91
Sequence 91, Application US/09903520
; Publication No. US2003054401A1
; GENERAL INFORMATION:
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Best Local Similarity 63.6%;
Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-09-902-692-91
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
                                CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-2
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
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PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
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Publication No. US20030054400A1
GENERAL INFORMATION:
APPLICANT Genentech, Inc.
APPLICANT Genentech, Inc.
APPLICANT Botterin, David
APPLICANT Botterin, David
APPLICANT Eacon, Dan L.
APPLICANT Ferrara, Napoleone
APPLICANT Ferrara, Napoleone
APPLICANT Fordy Sherman
APPLICANT Gerber, Hangpeter
APPLICANT Gerber, Hangpeter
APPLICANT Gerber, Hangpeter
APPLICANT Gerber, Hangpeter
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Grimaldi, Christopher J.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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PPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR PELICATION NUMBER: 09/665,350

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-13

PRIOR PELING DATE: 1999-13

PRIOR PELING DATE: 1999-10-6

PRIOR PELING DATE: 1999-10-6

PRIOR APPLICATION NUMBER: PCT/US99/2813

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-07

PRIOR PELI
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
         Botstein, David
                                        Desnoyers, Luc
Saton, Dan L.
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Best Local Similarity
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2002-01-22
CURRENT FILING DATE: 2000-02-22
PRIOR PEDICATION NUMBER: PCT/USOO/04414
PRIOR PEDICATION NUMBER: PCT/USOO/04414
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-12-02
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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Gao, Wei-Qiang
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493 GVSLSKLSLHN 503
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| PRIOR FILING DATE: 1999-12-20
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| PRIOR FILING DATE: 2000-01-05
| NUMBER OF SEQ ID NOS: 423
| SEQ ID NO 91
| LENGTH: 696
| TYPE: PRT
| ORGANISM: Homo @apiens
| US-09-905-056-91
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   Sequence 354, App Sequence 351, App Sequence 354, App Sequence 354, App Sequence 354, App Sequence 314, App Sequence 51, Appl Sequence 17, Appl Sequence 1344, Ap Sequence 1134, Ap Sequence 1134, Ap Sequence 11417, A Sequence 20956, A Sequence 20956, A Sequence 20956, A Sequence 1, Appli Sequence 20956, A Sequence 20954, A Sequence 1346, A
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                                                                                                        May 13, 2006, 08:26:32; Search time 28 Seconds (without alignments) 23.474 Million cell updates/sec
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US-11-188-298-1316

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Perfect
                                                                                                           Run on:
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No.
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Sequence 490, App Sequence 256, Appl Sequence 26, Appl Sequence 27, App Sequence 301, App Sequence 301, App Sequence 29040, A Sequence 20107, App Sequence 302, App Sequence 302, App Sequence 20107, App Sequence 20117, App Sequence 201

1 US-11-188-298-490
1 US-10-995-561-526
1 US-11-090-439-24
1 US-11-090-439-26
1 US-11-090-439-26
1 US-11-090-439-26
1 US-11-129-143-96
1 US-11-129-143-96
1 US-11-129-143-96
1 US-11-096-568A-29039
1 US-11-096-568A-29039
1 US-11-096-568A-29039
1 US-11-096-568A-29039
1 US-11-096-568A-26654
1 US-11-096-568A-28917
1 US-11-09

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341, App 14852, A 12274, A

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95 33 44.6 918 II US:11-079-463-6349 Sequence 423, App 463-6449 Sequence 424, App 463-6449 Sequence 6249, App 96 33 44.6 1445 II US:11-17-47-674 Sequence 719, App 96 33 44.6 1445 II US:11-17-47-672 Sequence 724, App 15 33 44.6 1445 II US:11-17-672 Sequence 726, App 17 33 44.6 1445 II US:11-17-672 Sequence 262, App 17 41.6 1444 II US:11-17-672 Sequence 262, App 17 444 II US:11-17-674 Sequence 262, App 17 444 II US:11-17
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APPLICANT: Gac, Wel-Quiang
APPLICANT: Gac, Wel-Quiang
APPLICANT: Gacdard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Austin L.
APPLICANT: Shorwood, Sreven
APPLICANT: Shorwood, Sreven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: APPLICANT: Watanabe, Tinnes, Daniel
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Tinnes, Daniel
APPLICANT: Stewart, Tinnes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Stewart, Tinnes, Daniel
APPLICANT: Stewart, T
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Sequence 231.4 Application US/10511538

Publication No. UB20060026700A1

GENERAL INFORMATION:
TITLE OF INVENTION: TESUE SPECIFIC GENES AND GENE CLUSTERS
FILE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
FILE REFERENCE: 16V 200 PCT
CURRENT APPLICATION NUMBER: US 60/312,669
PRIOR APPLICATION NUMBER: US 60/312,669
PRIOR APPLICATION NUMBER: US 60/411,882
PRIOR APPLICATION NUMBER: US 60/414,336
PRIOR FILING DATE: 2002-04-16
PRIOR PLICATION NUMBER: US 60/424,336
PRIOR FILING DATE: 2002-01-07
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-20
PRIOR FILING DATE: 2002-04-20
PRIOR FILING DATE: 2002-04-20
PRIOR FILING DATE: 2002-04-3
PRIOR FILING DATE: 2002-04-3
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-05
PRIOR PRIOR DATE: 2002-05-01
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Pred. No. 10;
4; Mismatches 0; Indels
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FILE REFERENCE: 39970-3330RIC300C1
CURRENT PELINON NUMBER: US/10/973,115B
CURRENT FILINO BATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 1002-05-14
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Best Local Similarity 63.6%;
Matches 7; Conservative '
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Deenoyers, Luc
APPLICANT: Filvaroff, Ellen
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493 GVSLSKLSLHN 503
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; ORGANISM: Homo sapiens
US-10-511-538-231
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PRIOR FILING DATE: 1997-09-19
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ORGANISM:
                                                                                                              TYPE: PRT
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APPLICANT:
APPLICANT:
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330NEC149
CURRENT PELLOCATION NUMBER: 108,10/137,873A
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: 60/049911
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Pred. No. 10;
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  PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION WUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-03-02
PRIOR APPLICATION WUMBER: US 60/135,736
PRIOR APPLICATION WUMBER: US 60/135,736
PRIOR APPLICATION WUMBER: US 60/135,736
PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 354
LENGTH: 696
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PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR PLING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PLING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.8%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
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Filvaroff, Ellen
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493 GVSLSKLSLHN 503
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                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-973-115B-354
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US-10-137-873A-354
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C407
                                                                                                                                                                                     Gaps
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550
SEQ ID NO 354
LENGTH: 696
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 354
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Pred. No. 10;
4; Mismatches
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                                                                                                                                                   Score 42; DB 9
Pred. No. 10;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Sequence 354, Application US/10152370; Publication No. US20060084139A1; GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Gurney, Austin L.
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                     Query Match 56.8
Best Local Similarity 63.6
Matches 7; Conservative
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493 GVSLSKLSLHN 503
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493 GVSLSKLSLHN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapien
US-10-152-370-354
                                                                                               ; ORGANISM: Homo Sapien
US-10-137-873A-354
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Gaps ö

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DB 11; Length 350;
                                                                           Score 37; DB 11; Length 310;
Pred. No. 35;
3; Mismatches 2; Indels
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; Sequence 54, Application US/11108528
; Publication No. US20050261189A1
; GENREAL INFORMATION:
   APPLICANT: Larsen, Glenn
   APPLICANT: Larsen, Glenn
   APPLICANT: Larsen, Glenn
   APPLICANT: Chen, C. M. Amy
   APPLICANT: Chen, C. M. Amy
   APPLICANT: Shamah, Steven M.
   TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
   TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
   TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
   TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CURRENT FILING DATE: 2004-04-18
   CURRENT FILING DATE: 2004-04-18
   PRIOR FILING DATE: 2004-04-16
   PRIOR FILING DATE: 2004-04-16
   PRIOR FILING DATE: 2004-04-16
   NUMBER OF SEQ ID NOS: 86
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 5: B
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APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.

APPLICANT: Chen, C. M. Amy
TITLE OF INVENTION: PROLIFFERATION
FILE REPERENCE: HYDR-POL-041
CURRENT APPLICATION NUMBER: US 60/563,137
RIOR APPLICATION NUMBER: US 60/563,137
RIOR APPLICATION NUMBER: US 60/598,368
FRIOR PLING DATE: 2004-04-16
FRIOR APPLICATION NUMBER: US 60/598,368
FRIOR RILING DATE: 2004-04-16
FRIOR APPLICATION NUMBER: US 60/598,368
FRIOR RILING DATE: 2004-04-16
FRIOR APPLICATION NUMBER: US 60/598,368
FRIOR RILING DATE: 2004-08-02
FRIOR APPLICATION NUMBER: US 60/598,368
FRIOR RILING DATE: 2004-08-02
FRIOR APPLICATION NUMBER: US 60/598,368
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49.3%; Score 36.5; I
Best Local Similarity 31.0%; Pred; No. 49;
Matches 9; Conservative 4; Mismatches
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135 VGFGEAISKQFVDALETGQDARAAMNLHN 163
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Publication No. US20050261189A1
GENERAL INFORMATION:
                                                                                Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                 3 YGMALSKINLH 13
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US-11-079-463-9199
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US-11-108-528-52
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TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOO-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-04-04
NUMBER: US SEQ ID NOS: 10444
NUMBER OF SEQ ID NOS: 10444
                                                                                                                                                                                                                                                                                                                                                                                                              PAPPLICANT: WOOG, WILLIAGH
APPLICANT: WOOG, WILLIAGH
APPLICANT: WOOG, WILLIAGH
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REPERENCE: P3330R1G21
FILE SAME
FILE SPERENCE: P3330R1G21
CURRENT APPLICATION NUMBER: US/11/290,153
CURRENT APPLICATION NUMBER: US/11/290,153
FRIOR PELING DATE: 1997-06-18
FRIOR PELING DATE: 1997-06-18
FRIOR PELING DATE: 1997-06-18
FRIOR PELING DATE: 1997-06-18
FRIOR PLING DATE: 1997-09-17
FRIOR PLING DATE: 1997-09-18
FRIOR PLING DATE: 1997-09-19
FRIOR PLING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-19
FRIOR PLING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-19
FRIOR PLING DATE: 1997-09-19
FRIOR FILING DATE: 1997-09-18
FRIOR PRIOR FILING DATE: 1997-09-18
FRIOR FILING DATE: 1997-09-18
FRIOR PRIOR FILING DATE: 1997-09-18
FRIOR FILING DATE: 1997-09-19
FRIOR FILING DATE: 1997-0
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56.8%; Score 42; DB 11; Length 696;

Best Local Similarity 63.6%; Pred. No. 10;

Matches 7; Conservative 4; Mismatches 0; Indels
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: Sequence 9199, Application US/11079463
: Publication No. US20060073161A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                          Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                    Tumas, Daniel
Watanabe, Colin K
Wood, William
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493 GVSLSKLSLHN 503
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CORGANISM: Homo Sapien
US-11-290-153-354
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ORGANISM: B.fragilis
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SOFTWARE: Patentin version 3.3
SEQ ID NO 2431
LENGTH: 532
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ROSE, MATTHIAS
VOSS, HAMUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5
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71 YGQALERLNLN 81
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-172-740-1344
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APPLICANT:
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                                                                     APPLICANT
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Sequence 17, Application Wo/11225903

Publication No. US2006005582A1

GENERAL INFORMATION:

APPLICANT: Feldmann, Kenneth A.

APPLICANT: Bobzin, Keneth A.

APPLICANT: Bobzin, Steven Craig

TITLE OF INVENTION: Modulation of Amino Acid and Sugar Content in Plants

FILE REPRENCE: 11666-137001/W01

CURRENT APPLICATION NUMBER: US/11/225,903

CURRENT FILING DATE: 2005-09-13

PRIOR APPLICATION NUMBER: 60/610,356

PRIOR APPLICATION NUMBER: 60/610,356

SEQ ID NO 17

LENGTH: 499

WADE A. PRO 17
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                                                      DB 11; Length 351;
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60.0%; Pred. No. 92;
tive 3; Mismatches 1; Indels
                                                                                         Indels
                                                                                           1;
                                                  Query Match 49.3%; Score 36.5; I Best Local Similarity 31.0%; Pred. No. 49; Matches 9; Conservative 4; Mismatches
                                                                                                                                                     :|:| |:||
136 VGPGEAISKQFVDALETGQDARAAMNLHN 164
                                                                                                                              1 MGYGMALSK-----INLHN 14
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; LOCATION: (1)...(499)
; OTHER INFORMATION: Public GI no. 11994438
US-11-225-903-17
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Publication No. US20060078901A1
GENERAL INFORMATION:
APPLICANT: BUCHRIESER, CARNEN
APPLICANT: COUNE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: PSIHI, HAFIDA
APPLICANT: DEHOUX, PIERRE
APPLICANT: GENOWA, PIERRE
APPLICANT: GENOWA, PIERRE
APPLICANT: GENOWA, PARID
APPLICANT: GENOWA, FARID
APPLICANT: GENOWA, FARID
APPLICANT: GLASER, PHILIPPE
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GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NG, EVA
VAZQUEZ-BOLAND, ANTONIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KUNST, FRANCK
COSSART, PASCALE
DANIELS, JUSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMEND, ALEXANDRA
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KREFT, JURGEN
KUHN, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||::||:
468 YGMAIADINM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YGMALSKINL 12
; ORGANISM: Homo sapiens
US-11-108-528-52
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                                                                                                                                                                                                                       RESULT 10
US-11-225-903-17
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APPLICANT:
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Sequence 1144, Application US/11172740

Sequence 1144, Application No. US20060057724A1

GENERAL INFORMATION:

APPLICANT: MASCIA, PETER

APPLICANT: ALEXANDROW, NICKOLAI

APPLICANT: ALEXANDROW, NICKOLAI

APPLICANT: BROVER, Vyacheslav

ITILE OF INVENTION: UNCLEDTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR

TITLE OF INVENTION: UNMBER: US/11/172,740

CURRENT FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 60/584,829

PRIOR APPLICATION NUMBER: 60/584,829

PRIOR PILING DATE: 2004-06-30

PRIOR PLING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

SEQ ID NOS: 2523

SEQ ID NO 1344
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TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
THE REPERENCE: 50394-0018-02
CURRENT APPLICATION NUMBER: 10/637,657
PRIOR PILING DATE: 2003-08-11
PRIOR FILING DATE: 2003-08-11
PRIOR FILING DATE: 2002-10-08
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
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HAIN, THORSTEN
BERCHE, PATRICK
CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Listeria monocytogenes US-11-045-004-2431
                                                                                                                                                                    GOMEZ-LOPEZ, NURIA
MADUENIO, ENCARNA
PABLOS, BETRIZ DE
WEHLAND, JURGEN
KARST, UWE
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RESULT 15
US-11-096-568A-20956
US-11-096-568A-20956
Sequence 20956, Application US/11096568A
Sequence 20956, Application US/11096568A
Sequence 20956, Application No. US20060048240A1
SERREAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theory
FILE REFERENCE: 2750-1592PBS
CURRENT TILLO DATE: 2005-04-01
SEQ ID NO 20956
SEQ ID NOS: 34471
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Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
47.3%; Score 35; DB 11; Length 332;
Best Local Similarity 30.8%; Pred. No. 89;
Matches 4; Conservative 6; Mismatches 3; Indels
                                                           Score 35; DB 11; Length 291;
Pred. No. 76;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11417, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION GENES AND USES FOR PLANT IMPROVEMENT
TITLE OF INVENTION GENES AND USES FOR PLANT IMPROVEMENT
TITLE OF INVENTION GENES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 11417
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAWE/KEY: misc_feature
; LOCATION: (1)..(332)
; OTHER INDEMATION: Ceres Seq. ID no. 12391420
US-11-096-568A-20956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                     47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 GHGISIGSLGVHN 171
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                                                                  Query Match 47.3
Best Local Similarity 60.0
Matches 6; Conservative
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192 IGYGLELSRI 201
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192 IGYGLELSRI 201
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                                                                                                                                                          1 MGYGMALSKI 10
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, ORGANISM: Glycine max US-11-188-298-5176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-11-188-298-11417
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US-10-698-618-1
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                                              FEATURE:
LOCALION:
LOCALION:
OTHER INFORMATION: Utility: Useful for increasing chlorophyll and photosynthetic cap
                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION:
COTHER INFORMATION: Utility: Useful for modifying fruit shape, composition and seed y
US-11-172-740-1344
                                                                                                                                                                                                      INFORMATION: Utility: Useful for making ornamental plants with modified leaves
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Utility: Useful for making plants with altered leaf shape eg curl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.3%; Score 35; DB 11; Length 226; 60.0%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1316, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENER AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(51452)8
CURRENT FILING DATE: 2005-07-22
FRIOR APPLICATION NUMBER: 60/592,978
FRIOR APPLICATION NUMBER: 60/592,978
FRIOR APPLICATION NUMBER: 60/592,978
FRIOR APPLICATION NUMBER: 60/592,978
FRIOR PELING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
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US-11-188-298-5176
Squence 5176, Application US/11188298
Squence 5176, Application US/11188298
Publication No. US200060075522A1
GENERAL INFORMATION.
TITLE OF INVENTION GENERS AND USES FOR PLANT IMPROVEMENT
FITLE OF INVENTION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 5176
IEBNOTH: 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
     LOCATION: (1)..(175)
OTHER INFORMATION: Public GI no. 2346976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j TYPE: PRT
; ORGANISM: Davidia involucrata
US-11-188-298-1316
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Best Local Similarity 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 MALSKINLHN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 MLLSKLNDHN 34
                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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US-11-188-298-1316
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Sequence 20954, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1532PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20954
LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-18-298-16346
); Sequence 16346, Application US/11188298
); Publication No. US20060075522A1
); GENERAL INFORMATION:
); APPLICANT: Abad, Mark S. et al.
); TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
); TITLE OF INVENTION UNMERR: US/11/188, 298
); CURRENT APPLICATION NUMBER: 60/592, 978
); PRIOR APPLICATION NUMBER: 60/592, 978
); PRIOR PILING DATE: 2004-07-31
); NUMBER OF SEQ ID NOS: 22569
); SEQ ID NO 16346
); LENGTH: 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

47.3%; Score 35; DB 11; Length 525;
Best Local Similarity 30.8%; Pred. No. 1.5e+02;
Matches 4; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452) B
CURRENT APPLICATION UNBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PLIING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 7401
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
| LOCATION: (1)...(525)
| LOCATION: (1)...(525)
| JOHER INDEMATION: Ceres Seq. ID no. 12391418
US-11-096-568A-20954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7401, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 GHGISIGSLGVHN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0°
Local 6; Conservative
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459 IGYGLELSRI 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-7401
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US-11-096-568A-20955
US-11-096-568A-20955
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WURENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SMOURENT FILING DATE: 2005-04-01
SMOURENT OF SEQ ID NOS: 34471
SEQ ID NO 20955
LENGTH: 502
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                                                                                                           APPLICANT: HAWMARSTROW, LARS
APPLICANT: HAWMARSTROW, CHRISTER
APPLICANT: LYNGSTADAAS, PETTER
APPLICANT: SLABY, IVAN
APPLICANT: SLABY, IVAN
APPLICANT: HAWMARGREN, TOWAS
ITILE OF INVENTION: WATERY PROTEIN COMPOSITIONS FOR WOUND HEALING
FILE REPERENCE: 4/927-48292-CPA
CURRENT APPLICATION NUMBER: US/10/698,618
CURRENT FILING DATE: 2003-10-30
PRIOR PILING DATE: 1093-02-26
PRIOR PELING DATE: 1999-02-26
PRIOR PILING DATE: 1999-02-26
PRIOR PILING DATE: 1999-0136
PRIOR PILING DATE: 1998-10-16
PRIOR PILING DATE: 1998-10-16
PRIOR PILING DATE: 1998-10-16
PRIOR PILING DATE: 1998-10-16
PRIOR PELING DATE: 1998-04-13
PRIOR PILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 9; Length 407; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(502)
; OTHER INFORMATION: Ceres Seq. ID no. 12391419
US-11-096-568A-20955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                        Sequence 1, Application US/10698618
Publication No. US20050271604A1
GENERAL INFORMATION:
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329 GHGISIGSLGVHN 341
                                                                                                    APPLICANT: GESTRELIUS, STINA
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70 LGFGKALNSLWLH 82
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGYGMALSKINLH 13
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ORGANISM: Rattus sp.
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US-11-096-568A-20954
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TYPE: PRT
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| Sequence 526, Application US/10995561
| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVACULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| CURRENT FILING DATE: 2004-11-24 |
| NUMBER OF SEQ ID NOS: 85702 |
| SEQ ID NO 526 |
| SEQ ID NO 526 |
| TINGTH 1404 
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Pred. No. 4.6e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 490, Application US/11188298
| Publication No. US20060075522A1
| Publication No. US20060075522A1
| GENERAL INFORMATION:
| APPLICANT: Abad, Mark S. et al.
| TYLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
| CURRENT TAPLICATION NUMBER: US/11/188,298
| CURRENT APPLICATION NUMBER: 05/592,978
| PRIOR FILING DATE: 2004-07-31
| NUMBER OF SEQ ID NOS: 22569
| SEQ ID NO 490
| LENGTH: 724
                                                                                                   Length 723;
                                                                                                       Score 35; DB 11; Length 72.
Pred. No. 2.2e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 47.3%; Score 35; DB 11; Best Local Similarity 60.0%; Pred. No. 2.2e+02; Matches 6; Conservative 3; Mismatches 1
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                                                                                                           Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGYGMALSKINLHN 14
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49 IGWGSQSSKVHIHH 62
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Best Local Similarity 35.7
Matches 5, Conservative
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515 IGYGLELSRI 524
                                                                                                                                                                                                                                                                                                                           517 IGYGLELSRI 526
                                                                                                                                                                                                                                                         1 MGYGMALSKI 10
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CORGANISM: Homo sapiens
US-10-995-561-526
; ORGANISM: Glycine max US-11-188-298-16346
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US-10-995-561-526
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US-11-188-298-490
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US-10-995-561-527
US-10-995-561-527
Sequence 527, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FITTLE OF INVENTION: DETECTION AND USES THEREOF
GURRENT APPLICATION UNDESS
CURRENT APPLICATION UNDESS
CURRENT FILING DATE: 2004-11-24
GURRENT FILING DATE: 2004-11-24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 527
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APPLICANT: Squillace, Rachel
TITLE Squillace, Nachel
TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
TITLE OF INVENTION: AUGUSTON NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR FILING DATE: 2006-03-25
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 24
SEQ ID NO 24
LENGTH: 1581
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Pred. No. 5.3e+02;
6; Mismatches 3; Indels
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Best Local Similarity 35.7%;
Matches 5; Conservative (
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; ORGANISM: Homo sapiens
US-11-090-439-26
                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-090-439-24
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us-10-769-514-17.rapbn

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3; Indels
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i_LOCATION: (1)..(365)
corres INFORMATION: Ceres Seq. ID no. 3599623
US-11.096-5688-29039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: misc_feature
| LOCATION: (1)...(344)
| PUTER INDRAMION: Ceres Seq. ID no. 3599624
US-11-096-568A-29040
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  Mismatches
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  1;
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 38.5%;
Matches 5; Conservative
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122 GYGIGSLTVNVHS 134
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  8; Conservative
                                            1 MGYGMALSKINL 12
                                                                   S IGYGKAHSKIIL 16
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US-11-096-568A-29039
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US-11-096-568A-29038
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Pred. No. 1.2e+02;
                                                                                                         Score 35; DB 9; Length 1588; 
pred. No. 5.3e+02; 
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.9%; Score 34; DB 9; Length 174; Best Local Similarity 36.4%; Pred. No. 65; Matches 4; Conservative 6; Mismatches 1; Indels
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Sequence 96, Application US/11129143

Publication No. US20050266518A1

GENERAL INFORMATION:

APPLICANT: BERTY, Alan

APPLICANT: HUBBELIN, Merner

APPLICANT: HUBBELIN, Markus

APPLICANT: LOPEZ-ULIBARN! Rual

APPLICANT: YELISEW, Alexei A.

TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION

FILE REPERENCE: C38435/121966

CURRENT APPLICATION NUMBER: US/11/129,143

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 197

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                         Sequence 301, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Mond, James
ITLE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 020349.9
PRIOR APPLICATION NUMBER: GB 020349.9
PRIOR APPLICATION NUMBER: GB 020349.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR APPLICATION NUMBER: GB 0200349.9
SRIOR APPLICATION NUMBER: GB 0200349.9
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; ORGANISM: Streptococcus pyrogenes
US-11-129-143-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus US-10-485-517-301
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                                                                                                           Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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49 IGWGSQSSKVHIHH 62
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81 YGLAIASLSVH 91
                                        , ORGANISM: Homo sapiens
US-10-995-561-527
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Best Local Similarity
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      LENGTH: 1588
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LENGTH: 292
                          TYPE: PRT
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Sequence 29040, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE REPERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 2940

LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29039, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29039
LENGTH: 365
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Pred. No. 1.5e+02;
4; Mismatches 4; Indels
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RESULT 35

US-11-079-463-8886

US-11-079-463-8886

Publication No. US20060073161A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WUGHER: US/11/079,463

CURRENT APPLICATION NUMBER: US/11/079,463

CURRENT PELLICATION NUMBER: US 60/128,705

PRIOR PELLICATION NUMBER: US 999-04-09

PRIOR PELLING DATE: 2000-04-04

NUMBER: US 99/540,209

PRIOR FILING DATE: 2000-04-04

NUMBER: US 99/540,209

FRIOR FILING DATE: 2000-04-04

NUMBER: US 99/540,209

FRIOR FILING DATE: 2000-04-04

SEQ ID NOS: 10444
                                                                                                                                                                                                                                                                                                                                     Sequence 7672, Application US/11079463
Publication No. US20060073161A1
GENERAL INFORMATION
APPLICANT GATY L. Breton
TITLE OF INVENTION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRACTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: PATHO0-031AV2
CURRENT PELLICATION NUMBER: US/11/079,463
CURRENT PELLICATION NUMBER: US 60/128,705
FRIOR PILLING DATE: 1999-04-09
FRIOR PILLING DATE: 1999-04-09
FRIOR PILLING DATE: 2000-04-04
FRIOR PILLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7572
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Pred. No. 2e+02;
2; Mismatches 1; Indels
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Pred. No. 2.3e+02;
1; Mismatches 2; Indels
Best Local Similarity 60.0%; Pred. No. 1.9e+02; Matches 6; Conservative 2; Mismatches 2; Indels
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US-11-188-298-3229
; Sequence 3229, Application US/11188298
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                       2 GYGMALSKIN 11
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; ORGANISM: B.fragilis
US-11-079-463-8886
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US-11-079-463-7672
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           APPLICAT: Alexandrov, Nickolai et al.
APPLICAT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-159,299102
CURRENT APPLICATION WHBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29038
LENGTH: 440
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US-11-188-298-7996
5-Sequence 7996, Application US/11188298
7-Sequence 7996, Application US/11188298
7-Experient No. US20060075522A1
7-EXPLICANT: ADAG, Mark S. et al.
7-TITE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
7-TITE OF INVENTION: 19425
7-EXPLICATION NUMBER: US/11/188,298
7-EXPRENT APPLICATION NUMBER: 00/592,978
7-EXPLICATION NUMBER: 60/592,978
7-EXPLICATION NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 32
US-11-087-099-8602
US-11-087-099-8602
| Sequence 8602, Application US/11087099
| Publication No. US20060041961A1
| GENERAL INFORMATION:
| APPLICANT: Abad, Mark S. et al.
| TILE OF INVENTION: Genes and Uses for Plant Improvement
| FILE REPRESENCE: 38-21(53450) B.P.
| CURRENT APPLICATION NHERR: US/11/087,099
| CURRENT PILING DATE: 2005-03-22
| NUMBER OF SEQ ID NOS: 12464
| SEQ ID NO 8602
| LENGTH: 445
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45.9%; Score 34; DB 11; Length 44
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5%; Pred. No. 1.98+02;
Matches 5; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

; LOCATION: (1)..(440)

OTHER INFORMATION: Ceres Seq. ID no. 3599622

US-11-096-568A-29038
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; ORGANISM: Butyrivibrio fibrisolvens
US-11-087-099-8602
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                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
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197 GYGIGSLTVNVHS 209
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45.9%; Score 34;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 34; DB 11; Length 724; 54.5%; Pred. No. 3.3e+02; Indels ive 3; Mismatches 2; Indels
APPLICANY: SHABLALLAN, ACLIANO
APPLICANY: SEKI, NACHIKO
APPLICANY: YOSHIKAWA, TSUTOMU
APPLICANY: YOSHIKAWA, TSUTOMU
APPLICANY: YOSHIKAWA, TSUTOMU
APPLICANY: YOSHIKAWA, TSUTOMU
APPLICANY: NACHARI, KENJI
APPLICANY: WASUHO, YASUHKO
TITLE OF INVENTION: Novel full length cDNA
TITLE OF INVENTION: NOVEL full length cDNA
FILE OF TRILING DATE: 2005-01-25
PRIOR PLILNG DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
SOFTWARE: PATENTIN VWHER: JF
SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2.1
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Sequence 46, Application US/11147047
PUBLICATION NO. US20050260668A1
GENERAL INFORMATION:
APPLICANT: Murdock, Paul R.
APPLICANT: Rizti, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Sinth, Randall F.
CURRENT PLING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US/10/21,097
PRIOR PLING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR PLING DATE: 2000-03-06
PRIOR PLING DATE: 2000-03-13
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-11-072-512-2224
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Sequence 308, Application US/10915002
Sequence 308, Application US/2060078950A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Handfield, Martin
APPLICANT: HOWING DESTINATION: DESTINATION: DESTINATION: DESTINATION: DISEASES
TILLE OF INVENTION: PERIODONTAL DISEASES
TILLE REFERENCE: 02-042
CURRENT APPLICATION NUMBER: US/10/915,002
CURRENT PAPLICATION NUMBER: 2004-08-10
NUMBER OF SEQ ID NOS: 354
SOFTWARE: PatentIn version 3.1
SEQ ID NO 308
LENGTH: 662
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Pred. No. 2.4e+02;
2; Mismatches 3; Indels
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              GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION:
FITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
SEQ ID NO 3229
LENGTH: 544
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Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUGIYAWA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative 5
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Best Local Similarity 75.0%;
Matches 6; Conservative
Publication No. US20060075522A1
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NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GMILTLVOLHN 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 GYGMALAQ 334
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US-11-072-512-2224
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RESULT 40

US-11-264-096-483

i Sequence 483, Application US/11264096

i Bequence 483, Application US/11264096

i Bedranka INFORMATION:

CERRERAL INFORMATION:

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE:

CURRENT PILLIG DATE: 2005-11-02

PRIOR APPLICATION NUMBER: US/11/264,096

CURRENT PAPPLICATION NUMBER: US/21/264,096

PRIOR APPLICATION NUMBER: 09/229, 358

PRIOR PILLING DATE: 2000-04-12

PRIOR PILLING DATE: 2000-04-12

PRIOR PILLING DATE: 2000-01-22

PRIOR PILLING DATE: 2000-04-25

PRIOR FILLING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1

CREATURE:

CREATURE:

CORGATION: (477)

CORGATION: (477)

CORGATION: (477)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-11-264-096-483
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4 GMALSKINLHN 14 | ||:::|| | 493 GTALTRINLRN 503

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Gaps

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Query Match
Best Local Similarity 54.5%; Score 34; DB 11; Length 845;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels

Search completed: May 13, 2006, 08:29:40 Job time : 29 secs

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S58062

AE0089

AE0089

S17089

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C7534
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                                                                             May 13, 2006, 08:10:22 ; Search time 39 Seconds (without alignments) 34.539 Million cell updates/sec
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Biocceleration Ltd.
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Maximum Match 100%
Listing first 100 summaries
              GenCore version
Copyright (c) 1993 - 2006
                                                          sw model
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B85481
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AH0057
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AR1533
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Gapop 10.0 , Gapext 0.5
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                                                                                                                          US-10-769-514-17
74
1 MGYGMALSKINLHN 14
                                                          protein search, using
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Maximum DB seq length: 200000000
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Query
Match Length DB
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906,
429,
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2338
89
204
1032
282
316
444
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627
603
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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Gaps

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ALIGNMENTS

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protein yaaH - Escherichia coli (strain K-12)
C;Species: Escherichia coli
DNA Seq. 3, 327-332, 1993
A;Title: Five open reading frames upstream of the dnaK gene of Escherichia coli.
A;Reference number: A56688; MUID:94003405; PMID:8400364
A;Reference number: A56688; MUID:94003405; PMID:8400364
A;Status: preliminary
A;Residues: 1-188 «JAM»
A;Residues: L-188 «JAM»
A;Residues: L-188 «JAM»
A;Residues: L-188 «JAM»
A;Reiference ranslated the codon ATT for residue 51 as Asn
B;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A;Reference number: A64720; MUID:97426617; PMID:9278803
A;Reference number: A64720; MUID:97426617; PMID:9278803
A;Reference number: A64720; MUID:97426617; PMID:9278803
A;Residues: 1-188 «ELAT»
A;Residues: 1-180 «ELAT»
A;Residues: 1-
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Accession: D80630
A;Accession: B90630
A;Rolecule type: DNA
A;Rolecul
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C;Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
C;Superfamily: Saccharomyces cerevisiae probable membrane protein C;Reywords: transmembrane #status predicted <TM1>
F;37-53/Domain: transmembrane #status predicted <TM3>
F;98-114/Domain: transmembrane #status predicted <TM3>
F;124-140/Domain: transmembrane #status predicted <TM3>
F;124-140/Domain: transmembrane #status predicted <TM3>
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Pred. No. 0.51;
2; Mismatches 4; Indels
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Matches 8; Conservative
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15 MGFGMTTILLNLHN 28
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                                                                                                                                                                                                              Conserved hypothetical protein STY0009 [imported] - Salmonella enterica subsp. enterica conserved hypothetical protein STY0009 [imported] - Salmonella enterica subsp. enterica conserved hypothetical protein subsp. enterica subsp. obean called Salmonella typhi

Z, Date: 09-Nov-2001

C, Date: 09-Nov-2001

R, Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, R.M.; Powd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.; Davis, R.M.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: ABDS02; MUID:21534947; PMID:11677608

A; Accession: ABDS03

A; Status; preliminary

A; Accession: ABDS03

A; Cross-references: UNIPARC:UPI000005996A; GB:AL513382; PIDN:CAD01162.1; PID:G16501292; C; Genetics: STY0009

C; Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
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B98441
Sp8461
Sp8cies: Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: B8840
NT.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
R;Perna, NT.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
R;Perna, NT.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
R;Perna, NT.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
R;Reture 409, 529-533, 2001
A;Ritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Referance number: A5480; MUID:21074935; PMID:11206551
A;Residues Serliminary
A;Molecule type: DNA
A;Residues ASTO
A;Residues ASTO
A;Residues ASTO
A;Genetice: Strain O157:H7, substrain EDL933
C;Superfemnily: Saccharomyces cerevisiae probable membrane protein FUN34
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B90630
B90630
C;Species [Similarity] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: 18-Jul-2004
C;Accession: K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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Pred. No. 0.51;
2; Mismatches 4; Indels
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Local Similarity 57.1%;
hes 8; Conservative 2
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MGFGMTTILLNLHN 28
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Length 119;

DB 2;

Score 43; DB 2 Pred. No. 1.1; 2; Mismatches

58.1%; 58.3%;

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A, Experimental source: strain Kl
C, Genetics:
A, Gene: APE1132
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Best Local Similarity 58...
7; Conservative
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77 GYGAGLSKVRVH 88
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Sep-1999
C;Accession: E72714
R;Kawarabayasi, Y:, Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
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A,Molecule type: DNA
A,Residues: 1-119 (KAW>
A,Cross-references: UNIPARC:UPI00005DE12; DDBJ:AP000060; NID:g5104188; PIDN:BAA80117.1;
           C;Accession: AH0057

R;Parkhil, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Recession: AH0057

A;Status: preliminary

A;Reliduas: 1-203 < KUR>
A;Reliduas: 1-203 < KUR>
A;Residuas: 1-203 < KUR>
A;Coss-references: UNIPROT:Q8ZIMB; UNIPARC:UP100000DC73D; GB:AL590842; PIDN:CAC89323.1;
C;Genetics:
A;Coss-references: Costevisiae probable membrane protein FUN34
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein VC0770 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug_2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: F82282
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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C;Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
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Pred. No. 0.55;
2; Mismatches 4; Indels
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Best Local Similarity 57.1%;
Matches 8; Conservative
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14 MGFGMTTILLNIHN 27
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-197 <HEI>
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Matches
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- Clostridı
                          C;Species: Clostridium acetoburylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Date: 14-Sep-2001
B;Accession: B96901
B;Accession: B96901
B;Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Bj Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Classeference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q97N28; UNIPARC:UPI00001390DC; GB:AE001437; PIDN:AAK77997.1, A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) ApaLI - Acetobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Acetobacter pasteurianus
Cispecies: Acetobacter pasteurianus
Cispecies: 15-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 31-Dec-2004
Cispeciesion: 15-96-1996 #sequence_revision 21-Jan-1997 #text_change 31-Dec-2004
Risucki, T.; Sugimoto, E.; Tahara, Y.; Yamada, Y.
Biosci. Biotechnol. Biochem. 60, 1401-1405, 1996
Biosci. Biotechnol. Biochem. 60, 1401-1405, 1996
A; Fitle: Cloning and nucleotide sequence of ApalI restriction-modification system from A; Reference number: JC4986; MUID:97141241; PMID:8987585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-429 <SUZ-
A;Cross-references: UNIPROT:P70750; UNIPARC:UPI00000B5146; DDBJ:D78276; NID:g1644233;
A;Experimental source: strain 1F013753
C;Comment: This enzyme belongs to cytosine-5 methylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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uncharacterized conserved protein, probable metal-binding CAC0010 [imported]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 17;
2; Mismatches 3; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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Best Local Similarity 58.3%;
Matches 7; Conservative
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142 MGYSVRLQKVNL 153
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Best Local Similarity 60..
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-906 <KUR>
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hypothetical protein ZK970.6 - Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: TZ8130
R;Berks, M.
R;Berks, M.
R;Berks, M.
R;Accession: TZ8130
A;Accession: TZ8130
A;Accession: TZ8130
A;Accession: TZ8130
A;Accession: TZ8130
A;Cession: TZ8130
A;Cession: TZ8130
A;Cession: TZ8130
A;Cession: TZ8130
A;Cession: Caemoria (CAEMOR)
C;Cention: Caemoria (CAEMOR)
C
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 173957, 156752, 773956
R;Matsushime, H.; Shibuya, M.
J. Virol. 64, 2117-2125, 1990
A;Title: Tissue-specific expression of rat c-ros-1 gene and partial structural similarit
A;Reference number: 156752; MUID:90219211; PMID:2139140
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A,Map position: 2
A;Introns: 28/3; 72/2; 153/2; 281/1; 312/3; 354/3; 401/1; 442/3; 660/3; 761/1; 819/2; 95:
C,Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-2338 <RES>
A;Cross-references: UNIPROT:Q63132; UNIPARC:UPI00000E793D; GB:M35106; NID:g203599; PIDN
A;Accession: 156752
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F733-737Domain: LDL receptor YWTD-containing repeat homology <YW3>
F1393-2214/Domain: procein kinase homology <KLN>
F1943-1951/Region: protein kinase ATP-binding motif
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Pred. No. 48;
2; Mismatches 0; Indels
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A43664
usg protein - Caulobacter crescentus
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Best Local Similarity 77.0
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Best Local 9
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                                Devo-Component sensor histidine kinase BH4026 [imported] - Bacillus halodurans (strain C-Species: Bacillus halodurans (species: Bacillus halodurans (species: Bacillus halodurans C-Species: Bacillus halodurans (species: Bacillus halodurans C-Species: Date: 0.1-bac-2000 #sequence_revision 01-bac-2000 #text_change 09-Jul-2004 (spacession: B84153 hakasons, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 hyritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Recreace number: A83650; MUID:20512582; PMID:11058132 hyracession: B84153 hyracession: B84153 hyracession: B84153 hyracession: B84153 hyracession: Bacillus halodurans and A; Residues: 1-607 cSTO> hyracesimences: UNIPROT:Q9K5R2; UNIPARC:UPI00000C439F; GB:AP001520; GB:BA000004; NID hyraces: BH4026
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A;Gene: XF2648 C;Superfamily: glutamyl-tRNA reductase

Ouery Match
Best Local Similarity Sv..
6; Conservative

220 GYALPLTELNIH 231

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2 GYGMALSKINLH 13

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Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative

|||| 221 MGYGDFSRKVNVHS 234 1 MGYGMALSKINLHN 14

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RESULT 12 T28130

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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N., O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                              A.Reference number: S74322; MUID:97061201; PMID:8905231
A.Accession: S74467
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Residues: 1-1032 «KAN»
A.Residues: 1-1032 «KAN»
A.Cross-references: UNIPROT:P72637; UNIPARC:UPI0000139F8B; EMBL:D90899; GB:AB001339; NIC
C.Genetics:
A.Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiNolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Jaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Barteriol. 181, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clay, Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: H97226
A;Status: preliminary
A;Molecule type: DMA
A;Redidues: 1-282 «KUR»
A;Cross-references: UNIPROT:Q97FS1; UNIPARC:UPIO0000CA5C9; GB:AE001437; PIDN:AAK80603.1,
B;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
A;Gene: CAC2656
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C;Species: Mycoplasma capricolum
C;Species: Mycoplasma capricolum
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S77783
R;Bork, P; Ouzounis, C; Casari, G; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W. Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolah, A;Reference number: S77739; MUID:96059641; PMID:7476192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein containing uncharacterized domain from NimC family [imported] - Clostridium ace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-316 < BOR>
A; Cross-references: UNIPROT: Q48999; UNIPARC: UPI00000B6594; EMBL: 233074; NID: 9516148;
A; Experimental source: ATCC 27343
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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A;Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 68;
1; Mismatches
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Pred. No. 25;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYGFTLSPVNL 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GYGMALSKINL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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C;Species: Caulobacter crescentus
C;Date: 03-Mar-1993 #text_change 09-Jul-2004
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A43664; H8768
R;Ross, C.M.; Winkler, M.E.
J; Bacteriol. 170, 757-768, 1988
A;Title: Structure of the Caulobacter crescentus trpFBA operon.
A;Reference number: A43664; MUID:88115177; PMID:2828322
A;Accession: A43664
A;Reference number: A43664; MUID:88115177; PMID:2828322
A;Accession: A43664
A;Reference number: A43664
A;Residues: 1-89 -ROS
A;Residues: 1-89 -ROS
A;Residues: 1-89 -ROS
A;Residues: 1-89 -ROS
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A887249; MUID:21173698; PMID:11259647
A;Reference number: A8872698.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: E69126
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliu, D.; Spadafora, R.; Vicainer, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Wierzbowski, J.; Gibson, R.; Jiwani, N. J. Bacteriol. 179, 7135-7155, 1997
J. Bacteriol. 179, 7135-7155, 1997
J. Recent Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reseion: E69126
A; Accession: E69126
A; Accession: E69126
A; Residues: 1-204 <ATH>A; Residues: 1-204 <ATH
A; Residues: 1-204 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI0000137E4F; GB:AE005673; NID:913425282; PIDN:AAK25508.1; C;Genetics:
A;Gene: CC3546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yaaH protein homolog MTH215 - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: E69126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Start codon: TTG
C;Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 4.6;
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Pred. No. 11;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.7%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.7%;
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LGFGITTILLNLHN 41
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11 MGYGLTTAEIHYH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.7
Best Local Similarity 46.2
Matches 6; Conservative
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Query Match 51.4%; Best Local Similarity 42.9%; Matches 6; Conservative

:|||: |::: || 284 IGYGVWLNRLYYHN 297 1 MGYGMALSKINLHN 14

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NyAlternate names: hypothetical protein F1913.26
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T00484; G84763
E;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsubited to the EMBL Data Library, April 1998
A;Description: Arabidopsis thaliana chromosome II BAC F1913 genomic sequence.
A;Reference number: 214160
A;Accession: T00484
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-627 cROU
A;Roos-references: UNIPROT:064766; UNIPARC:UPI00000A16AD; EMBL:AC004238; NID:g3033373;
A;Residues: 1-627 cROU
A;Roos-references: UNIROT:0610804
A;Residues: 1-627 cROU
A;Roos-references: UNIROT:0610804
A;Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Recession: G84763
A;Greesion: G84763
A;Greesion: G84763
A;Cross-references: UNIPARC:UPI00000A16AD; GB:AE002093; NID:g3033399; PIDN:AACI2843.1; G'Coss-references: UNIPARC:UPI0000A16AD; GB:AE002093; NID:g3033399; PIDN:AACI2843.1; G'Senerics: A;Generics: A;Generics: A;Map position: 2
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NyAlternate names: homeoric protein c1; homeotic protein Hox 2C; TATAA binding protein
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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Pred. No. 72;
1; Mismatches
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Best Local Similarity 81.8%;
Matches 9; Conservative
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TOSSIA
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Typotherical protein F23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32266
R;Wu, X.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F23F1.
A;Recernice number: 221142
A;Recernice number: 221142
A;Recession: T32266
A;Status: prealiminary; translated from GB/EMBL/DDBJ
A;Residues: 1-583 - WINX
A;Gene: CESP:F23F1.6
A;Amp position: A;Amp position: C;Genetics:
A;Introns: 88/2: 155/3; 199/3; 428/1; 509/3
C;Superfamily: ecotropic retrovirus receptor protein
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T004Berical protein At2g35030 [imported] - Arabidopsis thaliana
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Pred. No. 56;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 51.4%; Score 38; DB 2; Length 444; Local Similarity 70.0%; Pred. No. 41; 1. Indels 1; Conservative 2; Mismatches 1; Indels
                                                               Score 38; DB 2; Length 316;
Pred. No. 29;
5; Mismatches 3; Indels
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393 GICLSEINLH 402

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4 GMALSKINLH 13

Best Loc Matches

Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative ;

| ||||::|| 561 GQKLSKIDVHN 571

4 GMALSKINLHN 14

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A;Title: Expression of multiple homeobox genes within diverse mammalian haemopoietic lin
A;Reference number: S00987; MUID:88329001; PMID:2901346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 137-196 «KON»
A;Residues: 137-196 «KON»
A;Cross-references: UNIPARC:UP1000016CDEF; EMBL:X14570; NID:g51388; PIDN:CAA32708.1; PIF
R;Verrijzer, P.; de Graaff, W.; Deschamps, J.; Meijlink, F.
R;Verrijzer, P.; de Graaff, W.; Deschamps, J.; Meijlink, F.
R;Verrijzer, P.; de Graaff, W.; Deschamps, J.; Meijlink, F.
A;Title: Nucleotide sequence of the Hox2.3 gene region.
A;Reference number: 148411; MUID:88203221; PMID:2896332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPARC: UPI0000029981; EMBL: X06762; NID: 951389; PIDN: CAA29934.1; PI
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch., R.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari, E. A.; Entian, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, W.; Fuma, S.; Galizzi, A.; Galle, J.; Harwood, C.R.; Henaut, A.; Hibbert, M.; Holamphel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Latdinois A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, V.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Pottetell R; Rieger, M.; Riotlet, M.; Pamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, T.; Scanlon A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero akeuchi, M.; Tamakoshi, A.; Tanakao, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T; Minters P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tanaka, K.; Yasumoto, K.; Yata, K.; Yasu, K.; Anthors: Aparther and Parkers P.; Mipat, P.; Sumstein, E.; Yoshikawa, H.; Danchin, A.; Tanaka, K.; Yasumoto, K.; Yata, K.; Yasu, K.; Anthors: Aparther and Parkers P.; Mipat, P.; Shanchin, B.; Parkers P.; Aparther and Parkers P.; Parkers P.; Aparther and Parkers P.; Aparther P.; Apart
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C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 'LCV', 134-185, 'G', 187-205, 'H', 207-210,'A', 212-217 < LON>
A; Residues: 'LCV', 134-185, 'G', 187-205, 'H', 207-210, 'A', 212-217 < LON>
A; Residues: 'UNIPARC: UP100001745AD; EMBL:M18167
A; Note: the authors translated the codon CAG for residue 186 as Gly
A; Note: the authors translated the codon CAG for residue 186 as Gly
E; Kongsuwan, K.; Webb, E.; Housiaux, P.; Adams, J.M.
EMBO J. 7, 2131-2138, 1988
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C;Superfamily: Bacillus N-acetylmuramoyl-L-alanine amidase
P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt,
                                                                DNA 6, 409-418, 1987
A,Title: New murine homeoboxes: structure, chromosomal 8
A,Reference number: A29585; MUID:88054465; PMID:2890503
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29;
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Pred. No.
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Best Local Similarity
Matches 6; Conserv
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Nighternate names: homeoric protein Hox 2.3

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: A26846; B26846; B27176; A29585; S00988; 148411; S01887

R;Meijlink, F:, de Laaf, R:, Verrijzer, P:, Destree, O.; Kroezen, V.; Hilkens, J.; Desch Nucleic Acids Res. 15, 6773-6786, 1987

A;Title: A mouse homeobox containing gene on chromosome 11: sequence and tissue-specific A;Reference number: A26846

A;Reference number: A26846

A;Residues: 1-217 cMEL>
A;Residues: 1-217 cMEL>
A;Residues: 1-217 cMEL>
A;Residues: 1-217 cMEL>
A;Residues: BNA
A;Residues: 
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A; Residues: 1-217 <SIMA
A; Residues: UNIPROT: P09629; UNIPARC: UPI00001745A9; GB:MI6937
A; Norces the authors translated the codon GGC for residue 53 as Ala
R; Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc
Genome 31, 745-756, 1989
A; Title: Organization of human class I homeobox genes.
A; Reference number: S1535
A; Rcession: S1535
A; Rcession: S1535
A; Residues: 137-202 <BNA
A; Residues: 137-202 <BNA
A; Residues: 137-202 <BNA
A; Residues: 137-203 <BNA
A; Residues: 137-205 <
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossidues: 98-217 < MAL>
A;Cross-references: UNIPARC:UPI00001745AB; GB:S49765; NID:g233572; PIDN:AAB19469.1; PID:
A;Cross-references: UNIPARC:UPI00001745AB; GB:S49765; NID:g233572; PIDN:AAB19469.1; PID:
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:49765, NCBIP:49769)
C;Genetics: A;Gene: GB:HOKEN CMB: A;NOTE: CMB: A;NOT
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                     C;Accession: A28030; S15535; A44934
R;Simeone, A.; Mavilio, F.; Acampora, D.; Giampaolo, A.; Faiella, A.; Zappavigna, V.; D'
Proc. Natl. Acad. Sci. U.S.A. 84, 4914-4918, 1987
A;Title: Two human homeobox genes, cl and c8: structure analysis and expression in embry
A;Reference number: A28030; MUID:87260899; PMID:2885844
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A,Residues: 1-217 <ME2>
A,Crossareferences: UNIPARC:UPI0000029981; EMBL:Y00436; NID:g51387; PIDN:CAA68494.1;
R,Hart, C.P.; Fainsod, A.; Ruddle, F.H.
Genomics 1, 182-195, 1987
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A;Map position: 17q21.3-17q21.3
A;Introns: 134/1
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
P;138-194/Domain: homeobox homology <HOX>
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A;Cross-references: UNIPARC:UP100001745AC; EMBL:M18400
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; Pred. No. 29;
2; Mismatches
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Best Local Similarity 50.0
Matches 6; Conservative
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RESULT 30
A12206
hypothetical protein all3208 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Date: Nostoco sp. strain PCC 7120
C;Accession: A12206
A;Accession: A12208
C;Superfamily: Synechocystis hypothetical protein s1r1087
C;Superfamily: Synechocystis
A,Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A. A,Reference number: A84930; MUID:20445173; PMID:10993077
A;Reference number: A84963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <STO>
A;Coss.references: UNIPARC:UPI000005E514; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics: A;Gene: sobb; BU283
C;Superfamily: short protease IV-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispeciae; Archaeoglobus fulgidus
Cispeciae; Archaeoglobus
R.A.; Tomb, J.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R.K.E.; Clayron, R.A.; Tomb, J.F.; White, O.; Nelson, G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woose, C.X.; Venterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A,Authors: Hesson
A,Reference number: A69250; MUID:98049343; PMID:9389475
A,Accession: H69505
A,Accession: H69505
A,Accession: H69505
A,Accession: H69505
A,Accession: H69505
A,Residues: 1-378 - KLEs
A,CLES
A,Residues: L-378 - KLEs
A,CLOSS-references: UNIPROT:028230; UNIPARC:UPIO000056AAD; GB:AE000961; GB:AE000782; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 37; DB 2; Length 394;
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118 MGYGFARNCVNL 129
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165 GYGLAASQLN 174
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$27530

govulation protein - Clostridium acetobutylicum
C;Species: Of-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
R;Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
submitted to the EMBL bata Library, March 1992
B;Bestription: Cloning and sequencing of a spoilD gene from Clostridium acetobutylicum.
A;Reference number: S27530
A;Reteus: preliminary
A;Molecule type: DNA
A;Residues: 1-362 cRED.
A;Recosericies: UNIPROT:045833; UNIPARC:UP100000B7749; EMBL:M87835; NID:g144914; PIE
C;Superfamily: stage II sporulation protein D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable d-amino acid oxidase - fission yeast (Schizosaccharomyces pombe)
G/Species: Schizosaccharomyces pombe
G/Species: Schizosaccharomyces pombe
G/Species: Schizosaccharomyces pombe
G/Accession: T40989
Striyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
Submitted to the EMBL Data Library, March 1999
A/Recession: T40989
A/Recession: T40989
A/Residues: 121962
A/Residues: 1-348 c.LYN
A/Residues: 1-348 c
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A84963
probable proteinase sobB [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: A84963
R;Shigenobu, S.; Watenabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0%; Score 37; DB 2; Length 362; Best Local Similarity 53.0%; Pred. No. 51; Matches 7; Conservative 2; Mismatches 4; Indels
                                                            Score 37; DB 2; Length 250;
Pred. No. 34;
2; Mismatches 4; Indels
                                                       Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 2
                                                                                                                                                                                                                                  2 GYGMALSKINLHN 14
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18 GYAMAPAYITVHN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GYGMALSKINLHN 14
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Query Match Best Local S Matches 7

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A; Molecule type: DNA
A; Residues 1-691 acuta
A; Experimental source: strain HR3
A; Experimental source: strain HR3
A; Experimental source: strain HR3
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
B; Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
Virology 202, 586-605, 1994
A; Fitle: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus
A; Reference number: A72850; MUID:94303173; PMID:8030224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1.692 «KAM»
A;Cross-references: UNIPROT:092464; UNIPARC:UPI0000F9A16; EMBL:L33180; NID:g3745835; P
A;Experimental source: isolate T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA recombinase (EC 3.6.1.-) - Escherichia coli (strain K-12)

NyAlternate names: RecG protein

NyAlternate names: RecG protein

CjSpecies: Bacherichia coli

CjSpecies: Bacherichia coli

CjAccession: JH0265; S18195; F65166

CjAccession: JH0265; S18195; F65166

R;Kalman, M.; Murphy, H.; Cashel, M.
Gene 110, 95-99, 1992

A;Title: The nucleotide sequence of recG, the distal spo operon gene in Escherichia col

A;Reference number: JH0265; MUID:92184121; PMID:1544582
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaiduea: 1-691 <AYR>
A;Cross-references: UNIPARC:UP10000138C95; GB:L22858; NID:9510708; PIDN:AAA66734.1; PID
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R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus. A;Reference number: Z22020; MuID:99281911; PMID:10355780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 67.2-68.5
C,Superfamily: baculuovizus p87 capsid protein
C,Keywords: capsid protein; glycoprotein
F;2,71,102,319/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T41845
VP80 orf104 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
A; Reference number: A43376; MUID: 92410596; PMID: 1529529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: vp80
C;Superfamily: baculovirus p87 capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
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527 YGSLLKRLNLYN 538
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: DNA
                                      A; Accession: A43376
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A; Molecule type: DNA
A; Residues: 1-531 «FELD
A; Residues: 1-551 «FELD
A; Cossereferences: UNIPARC: UP1000006B390; EMBL: Z74797; NID: g1419864; PID: e251864; PID: g
A; Experimental source: strain S288C
B; Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
Bubmitted to the EMBL. Data Library, August 1995
A; Description: Analysis of a 26kb region on the left arm of yeast chromosome XV.
A; Reference number: S59285
A; Molecule type: DNA
A; Residues: 1-543 «FEM>
A; Molecule type: DNA
A; Residues: 1-543 «FEM>
A; Cossereferences: UNIPARC: UP1000006ACE0; EMBL: X91067; NID: g984187
B; Mannhaupt, G; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
Yeast 12, 67-76, 1996
A; Title: Analysis of a 26 kb region on the left arm of yeast chromosome XV.
A; Reference number: 861715; MUID: 96381248; PMID: 879261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: S61724
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Moses-references: UNIPARC:UPI000006ACE0; EMBL:X91067; NID:g984177; PIDN:CAA62531.1; PI
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C,Genetics:
C,Genetics:
A,Gene: SGD:TH120
A,COSS-references: SGD:S0005416
A,Map position: 15L
                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S66740; S66747; S59294; S61724
R;Ancession: W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S. submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Reference number: S66740
A;Accession: S66740
A;Accession: S66740
A;Residues: 1-551 cANS>
A;Residues: 1-551 cANS>
A;Cross-references: UNIPROT:Q08224; UNIPARC:UPI00006B390; EMBL:Z74797; NID:g1419864; PI
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Pred. No. 81;
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R,Feldmann, H.; Manhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, July 1996
A,Reference number: $66743
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         Pred. No. 56;
5; Mismatches
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70.0%;
         50.0%;
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286 LGFGVALFKVSL 297
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                                         6; Conservative
                                                                                                  1 MGYGMALSKINL 12
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         Best Local Similarity
Matches 6; Conserv
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Depochetical protein recG [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C.Species: Escherichia coli (Species: Escherichia coli O157:H7: Plunkert III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew! S., Potamousis, K.; Apodaca, Iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.; Tite Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.; Tite Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A.; Tite Grocheck, E.J.; Potamousis, K.; Apodaca, A.; Tite Grocheck, E.J.; Potamousis, K.; Apodaca, A.; Tite Grocheck, E.J.; Potamousis, K.; Apodaca, A.; Escherica Preliminary
A.; Molecule type: DNA
A.; Escherica Preliminary
A.; Escherica Prelim
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C; Species: Agrobacterium Tumefaciens
C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: H97238
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A12747
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-809 KURN-
A;Cross-references: UNIPROT:QSUFK4; UNIPARC:UPI00001645E0; GB:AE008688; PIDN:AAL42399.1,
A;Experimental source: strain C58 (Dupont)
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A;Map position: circular chromosome
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A,Accession: JH0265
A,Accession: JH0265
A,Accession: JH0265
A,Accession: JH0265
A,Riber Lega (Rib.)
A,Cross-references: UNIPROT:P24230; UNIPARC:UPI000003EB2A; GB:M64367; NID:G147543; PIDN: A,Experimental Source: strain K12
R,ILDVd, K.G.; Sharples, G.J.
J, Bacteriol. 173, 6313-6843, 1991
A,Fillow, M.G.; Sharples, G.J.
A,Accession: S18195
A,Accession: Man, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Atle: The complete genome sequence of Escherichia coli K-12.
A,Accession: F65166
A,Ac
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G191194

BNA helicase RecG [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C, Species: Bscherichia coli
C, Date in 18-011-2001 #sequence_revision 18-011-2001 #text_change 09-01-2004

C, Accession: G91194

R, Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A, Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A, Recession: G91194

A, Reseidus: preliminary
A, Molecule type: DNA
A, Residuss: 1-693 < HAY>
A, Residuss: 1-693 < HAY>
A, Reseiduss: 1-693 < HAY>
A, Conserved Rome Recession (157:H7) & Substrain RIMD 0509952
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C;Superfamily: DNA helicase recG
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A;Molecule type: DNA
A;Residues: 1-168 <STO>
A;Cross-references: UNIPROT:Q917A8; UNIPARC:UPI000012915C; GB:AE004441; GB:AE004091; NIC
C;Genetics:
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999
B;Cacession: F7259
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUD:99310339; PMID:10382966
A;Accession: F7259
A
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C;Cates: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83643
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
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A;Accession: H83643
                                    A; Accession: H97528
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-873 < KUR>
A; Cross-references: UNIPROT:Q8UFK4; UNIPARC:UPI00000D1B38; GB:AE007869; PIDN:AAK87185.1;
C; Genetics:
A; Genetics:
A; Map position: circular chromosome
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A; Reference number: A97359; MUID:21608551; PMID:11743194
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=480;
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TAAH ECOLI

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OT 01-085-1992

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REMBL, AR039314; AAC3479.1; -; Genomic_DNA.

GO; GO:00046026; Cimembrane; IEA.

GO; GO:00046026; Cimembrane; IEA.

GO; GO:0016026; Cimembrane; IEA.

DR GO; GO:0016026; Transferrin bind.

PR Ffam; PF01298; Lipoprotein 5; 1

SGUENCE 706 AA; 76492 WW; FB817A285958E64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-4223;

WEDLINE-98380363;

Where L.E., Yang Y.D., Wang Q., Harkness R.E.,

Schryvers A.B., Klein M.H., Loosmore S.M.;

Schryvers A.B., Klein M.H., Loosmore S.M.;

Schryvers A.B., Klein M.H., Loosmore S.M.;

The transferrin binding protein B of Moravella catarrhalis elicits

bactericidal antibodies and is a potential vaccine antigen.";

Infect. Immun. 66:4183-4192(1998)

EMBL; ARC34277; 1: , Genomic_DNA.

GO; GO:0016020; C:membrane; I.B.,

GO; GO:004998; F:transferrin receptor activity; IEA.

InterPro; IPR001677; Transferrin_bind.

Pran; PR01298; Lipoprotein_5; I.

SEQUENCE 702 AA; 75458 MW; 974CBC14BBB0555A CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 26, Last annotation update)
1ransferrin binding protein B.
Noracalla catarhalis.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Noraxallaceae; Moraxella.
NOTAXALIBAGEAE;
NOTAXALIBAGEAE;
NOTAXALIBAGEAE;
NOTAXALIBAGEAE;
NOTAXALIBAGEAE;
                                                                                                                      085050.

01-NOV-1998 (TEMBLE-108, Carated)

01-NOV-1998 (TEMBLE-1). 08, Last sequence update)

01-MAR-2004 (TEMBLE-1). 08, Last annotation update)

Transferrin binding protein B.

Noraxella catarrhalis.

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Noraxellaceae; Noraxella.

NORAXELIACEAE; Noraxella.
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                                                                                                 702 AA
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                                                         0085050_MORCA PRELIMINARY;
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085052;
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NUCLEOTIDE SEQUENCE.
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080052 MORCA
080052 MORCA
AC 085052 M
DT 01-NOV-1;
DT 01-NOV-
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Matches
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MEDLINE=9380053;
MEDLINE=9380053;
MEDLINE=9380053;
Pubmed=9712766;
Myers L.E., Yang Y.P., Du R.P., Wang O., Harkness R.E.,
Schrywers A.B., Klein M.H., Loosmore S.M.;
The transferrin binding protein B of Moraxella catarrhalis elicits
bactericidal antibodies and is a potential vaccine antigen.";
Infect. Immun. 66:4183-4192 (1998).
EMBL; AR039316; AA034283.1; -; Genomic_DNA.
GO; GO:0016020; C.membrane; IEA.
GO; GO:0016020; C.membrane; IEA.
GO; GO:0016020; T.ransferrin receptor activity; IEA.
FIREPPRO: IRROGAT7; Transferrin.bind.
Pfan; PF01298; Lipoprotein S; 1...
SEQUENCE 714 AA; 76846 WW; F5B1174C4815E4EA CRC64;
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P28655; 08KN72;
01-DEC-1992 (Rel. 24, Created)
101-DEC-1992 (Rel. 24, Last sequence update)
101-DEC-1992 (Rel. 24, Last sequence update)
101-DEC-1992 (Rel. 24, Last annotation update)
101-SEP-2005 (Rel. 48, Last annotation update)
101-SEP-2005 (Rel. 24, Last annotation update)
101-SEP-2005 (Rel. 24, Last sequence update)
101-SEP-2005 (Rel. 24, Last annotation 
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NUCLECTIDE SEQUENCE.
SPECIES-E.COli;
MEDLINE=94003405; PubMed=8400364;
James R., Dean D.O., Debbage J.;
Five open reading frames upstream of the dnaK gene of E. coli.";
DNA Seq. 3:327-332(1993).
                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Moraxella.
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                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transferrin binding protein B.
714 AA.
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PRIX. BS0630; BS0630.

PIR; BS0630; BS0630.

PIR; ES0681 ES0688.

ECOGEN: EB1112; yaaH.

ECOGEN: FR0007911 Grp1 Fun34 YaaH.

ProDom; PF01184; Grp1 Fun34 YaaH; 1.

ProPo_DOM Fun34 YaAH; 1.

Complete proteome; Inner membrane; Membrane; Transmembrane.

TOPO_DOM (Potential).
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Periplasmic (Potential).
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               X67700; CAA47931.1; -; Genomic_DNA.
D10483; BAB96588.1; -; Genomic_DNA.
AE00096; AAC73121.1; -; Genomic_DNA.
BA000007; BAB313.1; -; Genomic_DNA.
BA000007; BAB3433.1; -; Genomic_DNA.
AE016978; AAN11556.1; -; Genomic_DNA.
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20071 MW;
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Matches 8; Conservative
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PubMed=15781495;
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TOPO DOM
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                    EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

SPECIES=E.coli, STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.,

"Complete genome aequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.flexneri, STRAIN=301 / Serotype 2a;
SPECIES=S.flexneri, STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12385590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 308:1321-1323 (2005).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the GPR1/FUN34/yaaH family.
               WÜCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
SPECIES=E.coli, STRAIN=K12 / MG1655,
MEDLINE=97426617, PubMed=9278630, DOI=10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perra N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRECIES=E.coli; STRAIN=K12 / MG1655;
PubMed=15919996; DOI=10.1126/science.1109730;
Daley D.O., Rapp M., Granseth E., Melen K., Drew D., von Heijne G.;
"Global topology analysis of the Escherichia coli inner membrane
                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074935; PubMed=11205551; DOI=10.1038/35054089;

MEDLINE=210.74935; PubMed=11205551; DOI=10.1038/35054089;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hacket J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Lin J., Yen G., Schwartz D.C., "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

SPECIES=S.flexneri; STRAIN=24577 / ATCC 700930 / Serotype 2a;

SPECIES=S.flexneri; STRAIN=24577 / ATCC 700930 / Serotype 2a;

BEDINES-2559074; PubMed-12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A.,

Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

Schwartz D.C., Blattner R.R.;

Complete genome sequence and comparative genomics of Shigella

flexneri serotype 2a strain 2457T.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteome.
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Wang H.-S., Lee Y.-S.;
Wang H.-S., Lee Y.-S.;
Why sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistant zoonotic pathogen.";
Nucleic Acids Res. 33:1690-1698(2005).

EMBL, AE017220, AAX63915.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative regulator.
Name-yaaH; OrderedLocusNames=SC0009;
Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                            Score 46; DB 1; Length 188;
Pred. No. 6.4;
                                                                                                                                                                     4; Indels
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Cytoplasmic (Potential).
L -> V (in Ref. 2).
972101DD5949EBF4 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA
                                                                                                                                                                  2; Mismatches
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Matches 8; Conservative
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TO NOTECTION SEQUENCE.

TO NOT
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OR-2003 (TrEMBLrel. 23, Last sequence update)
01-OR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein yaaH.
Name-yaaH; OrderedLocusNames=c0015;
Escherichia ooli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                h 62.2%; Score 46; DB 2; Length 188; Similarity 57.1%; Pred. No. 6.4; 8; Conservative 2; Mismatches 4; Indels
Nature 413:852-856(2001).
Nature 413:852-856(2001).
Nature 413:852-856(2001).
SWBL, AE008693; AAL18973.1; -; Genomic_DNA.
GO, GO:0016020; C:membrane; IEA.
InterPro; IPR000791; Grpl. Fun34_YaaH.
ProDom; PD010188; Grpl. Fun34_YaaH; 1.
ProDom; PD01114; GFR1_Fun34_YaaH; 1.
Complete Protecome.
Complete 188 AA; 19933 MW; 4D655AC780BBB808 CRC64;
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8; Conservative
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15 MGFGMTTILLNLHN 28
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QBFLC8;
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Best Local Similarity
Matches 8; Conserv
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MEDLINE-21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M. Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Acceptor R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OS-UTL.2004 (TrEMBLrel. 27, Created)
OS-UTL.2004 (TrEMBLrel. 27, Last sequence update)
OS-UTL.2004 (TrEMBLrel. 27, Last sequence update)
OS-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Putative regulatory protein.
Name=yaaH; OrderedLocusNames=STM0009;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Brierobacteriaceae; Salmonella.
                                                                                                                                                                                               01-FEB.2005 (TrEWBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last asquence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Name=yaaH; OrderedLocusNames=SPA0009;
Salmonella paratyphi-a.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.2%; Score 46; DB 2; Length 188; Best Local Similarity 57.1%; Pred. No. 6.4; Matches 8; Conservative 2; Mismatches 4; Indels
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| HGFGMTTILLNLHN 28
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07CRA2;
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        MGYGMALSKINLHN
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Gaps
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OBKGES, Q'ANMES,
OBKGES, Q'ANMES,
O1-MAR-2002 (TERMELEI. 20, Last sequence update)
O1-MAR-2002 (TERMELEI. 20, Last sequence update)
13-SEP-2005 (TERMELEI. 2), Last amnotation update)
Hypothetical protein yanH (Hypothetical protein STY0009).
Name-yaH; OrderedLocusNames=STY0009, t0009;
Salmon-la typhi.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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62.2%; Score 46; DB 2; Length 188; 57.1%; Pred. No. 6.4; ive 2; Mismatches 4; Indels
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GO:0016020; C:membrane; IEA.
                                                                                              Complete proteome. SEQUENCE 189 AA;
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Best Local Similarity
Matches 8; Conserv
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Q74Q11_YER
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                                                                          STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                               MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
Whitchead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica servora Typhi CT18";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2225/627, PubMed=14528314; DOI=10.1038/nbt886; Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Ende C., Chandler M., Charles J.-F., Dassas E., Derose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Signier P., Vincent R., Wingate V. Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.; "The genome sequence of the entomopathogenic bacterium Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Photorhabdus luminescens (subsp. laumondil),
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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EMBL; AL627265; CAD01162.1; -; Genomic_DNA.
EMBL; AL627265; CAD01162.1; -; Genomic_DNA.
CO; GO:0016020; C::membrane; IEA.
InterPro; IPR000791; Grpl Pun34 YaaH.
ProDom; PP010188; Grpl Pun34 YaaH; 1.
PROSITE; PS01114; GRpl FUN34 YAAH; 1.
COMplete protecome; Hypothetical protein.
SEQUENCE 188 AA; 19933 MW; 4D655AC780BBB808 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
similar to unknown protein YaaH of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 AA.
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Pred. No. 6.4;
2; Mismatches
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EMBL; BX571860; CAE12873.1; -; Genomic_DNA.
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            Enterobacteriaceae; Salmonella,
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57.1%;
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Query Match

Best Local Similarity 57...,

Best Conservative

The Conservative
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                                 NCBI_TaxID=601;
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Pall K.S., Sebaihia M.R. Partchard L., Holden M.T.G., Hyman L.J.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
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                                                                                                                                  Length 189;
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                                                                                        189 AA; 20289 MW; E9D5C44D35306A7F CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                  Score 46; DB 2;
Pred. No. 6.4;
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InterPro; IPR000791; Grp1 Fun34 YaaH.
Pfam; PF01184; Grp1 Fun34 YaaH; 1.
ProDom; PD010188; Grp1 Fun34 YaaH; 1.
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074011;
05-JUL-2004 (TERMELRE1. 27, C:
05-JUL-2004 (TERMELRE1. 27, L:
05-JUL-2004 (TERMELRE1. 27, L:
PLATIVE MEMBRANE PROTEIL:
OrderedLocusNames=YP3713;
                                                                                                                                     62.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Putative membrane protein. OrderedLocusNames=ECA3883;
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MGFGMTTILLNLHN 28
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                                                                                                                                                                                  8; Conservative
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NUCLECTILES SAUGMANEL.

STRAIN=KINS / Biovar Mediaevalis;

RX DALINE=22137863; PubMed=12142430;

RX DOI=10.1126/JB.184.16.4610.02;

RX DOI=10.1126/JB.184.16.4610.02;

RA Derna W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,

RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

RA Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RY Genome sequence of Yersinia pestis KIM.";

RY "Genome sequence of Yersinia pestis KIM.";

LJ. Bacteriol. 184:4601-4611(2002).

BRBL; A414142; CAC69323.1; -; Genomic_DNA.

BRBL; A414142; CAC69323.1; -; Genomic_DNA.

BRBL; A40057; A40057.

RY A40057; A40057.

RY A40057; PRO00791; Grpl. Fun34. YaaH.

RY PEDPON; POLO16020; C.membrane; IRA.

RY PEDPON; POLO16020; C.membrane; IRA.

RY PEDPON; POLO184; Grpl. Fun34. YaaH;

RY PEDPON; POLO184; Grpl. Fun34. YaaH;

RY Complete proteome; Hypothetical protein.

SQ SEQUENCE 203 AA; 21661 MW; 200282B6691CD661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CO-92 / Biovar Orientalis; STRAIN=CO-92 / Biovar Orientalis; STRAIN=CO-92 / Biovar Orientalis; STRAIN=CO-92 / Biovar Dished=11586360; DOI=10.1038/35097083; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Partice M.B., Sebalhia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Leatherl T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Stalton J., Stevens K., Whitehead S., Barrell B.G.; Mature 413:523-527(2001).
QBZIMB_YERPE PRELIMINARY; PRT; 203 AA.

QBZIMB_QCGTER_CONCTEMBLE. 20, Created)
01-MAR-2002 (TrEMBLE. 20, Last sequence update)
01-MAR-2002 (TrEMBLE. 20, Last sequence update)
01-FEB-2005 (TrEMBLE. 20, Last annotation update)
Putative membrane protein (Hypothetical protein y3707).
Name-yaaH; OrderedLocusNames=YPO0467, y3707;
Yersinia pestia.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Best Local Similarity 5/...
Best Local Similarity 5/...
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=632;
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NOTICE STRAIN—S2 / LL;

Nubled=1546649; DO=10.1128/JB.186.20.6956-6969.2004;

Nubled=1546649; DO=10.1128/JB.186.20.6956-6969.2004;

Nubled=1546649; DO=10.1128/JB.186.20.6956-6969.2004;

Nubled=1546649; DO=10.1128/JB.186.20.6956-6969.2004;

Nubled=1546649; DO=10.1128/JB.186.20.6956-6969.2004;

Nubled=1546649; DO=10.1128/JB.186.20.6956.6099;

Nubled=1546649; Dozat I.; Palmeirl A.; Rouse G.;

Nubled=1546649; Dozat I.; Palmeirl A.; Rouse G.;

Nubled=1546649; Dozat I.; Van Dien B.; Wang T.; Whitman W.B.;

Nubled=1546649; Nubled=15466; Nubled=154649; Nubled=154669; Nubled=154696; Nubled=154696; Nubled=154696; Nubled=154696; Nubled=154696; Nubled=154696; Nubled=154696; Nubled=1546999; Nubled=154696; Nubl
                                                                                                                                                             Scong Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D., Zhou D., Oin H., Pang X., Han Y., Zhai J., Li M., Cui B., Oi Z., Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin M., Wang J., Yu J., Yang H., Wang H., Wang H., Wang P., Yang R., "Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans."

"Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans."

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent Yersinia pestis strain 91001, an isolate DNA Res. 11:179-197(204).

"Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent Yersinia pestis strain 91001, an isolate description of Yersinia pestis strain 91001, an isolate description of Yersinia pestis strain 91001, an isolate description of Yersinia pestis strain 91001, A. Yersinia description of Yersinia pestis strain 91001, A. Yersinia description of Yersinia pestis strain 91001, A. Yersinia description of Yer
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Pred. No. 6.7;
2; Mismatches 4; Indels
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62.2%; Score 46; DB 2; Length 196;
Best Local Similarity 57.1%; Pred. No. 6.6;
Matches 8; Conservative 2; Mismatches 4; Indels
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Q6MOC3;
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Best Local Similarity 57.1
Matches 8; Conservative
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                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                            STRAIN=91001;
PubMed=15368893;
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Gaps
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pubMed=1535886; DOI=10.1073/pnas.0404012101;
Châin P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
                                                                                                                                                                                                                              25.0CT-2004 (TrEMBLrel. 28, Created)
25.0CT-2004 (TrEMBLrel. 28, Last sequence update)
25.0CT-2004 (TrEMBLrel. 28, Last annotation update)
25.0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative regulator; integral membrane protein.
Name=yaaH; OrderedLocusNames=YPTB0610;
Persinia pseudotuberculosis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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0
Score 46; DB 2; Length 203;
Pred. No. 6.9;
2; Mismatches 4; Indels
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                                                                           1 MGYGMALSKINLHN 14
                                                                                                15 MGFGMTTVLLNLHN 28
                                                                                                                                                                                                  QGGET1 YERPS PRELIMINARY;
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21 MGFGMTTVLLNLHN 34

RESULT 14 Q8ZIM8_YERPE

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Pubmed-1507118; DOI=10.1038/nbt959;

Pubmed-15077118; DOI=10.1038/nbt959;

Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,

A Rolonay J.F., Elsen J.A., Ward N.L., Methe B.A., Brinkac L.M.,

Daugherty S.C., DeBoy R.T., Dadson R.J., Durkin A.S., Madupu R.,

A Daugherty S.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Davidson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Perdbhyum T.V., Wall J.D., Voordouw G., Fraser C.M.;

The genome sequence of the anaerobic, sulfate-reducing bacterium

Desulfovibrio vulgaris Hildenborough.";

Nat. Bactechnol. 22:554-559(2004).

REBL: ABCITTISH; AAS97261.1; -; Genomic_DNA.

RIGK; DVUZ789; - (Rembrane; IEA.)

RIGK; DVUZ789; - (Rembrane; IEA.)

RIGK; POUZ789; GTPL FUN34_YaaH.

REPOM; POUR184; GTPL FUN34_YaaH; 1.

REPOM; POUR184; GTPL FUN34_YaaH; 1.
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STRAIN=LSV54 / DSM 12343;
PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.;
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from microbiol. 6:887-902 (2004).

BNBL; CR522870; CAG3748.1; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

InterPro; IPR000791; Grpl_Fun34_YaaH.
                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfotalea.
                                                                                                                                                                                                   Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.5%; Score.44; DB 2; Length 183; 50.0%; Pred. No. 14; tive 3; Mismatches 4; Indels
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25-077-2004 (TrEMBLrel. 28, Last sequence update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
Conserved hypothetical membrane protein.
OrderedLocusNames=DP2519;
                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Gprl/Fula4/YaaH family protein.
OrderedLocusNames=DVU2789;
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                         Q727R6_DESVH ID Q727R6_DESVH PRELIMINARY;
AC Q727R6;
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nes 7; Conservative
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PubMed=15044751; DOI=10.1126/science.1094786;
Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
Lancto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
Anantharaman V., Aravind L., Kapur V.;
"Complete genome sequence of the apicomplexan, Cryptosporidium
Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L., Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C., Simoner M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M., Derbise A., Hauser L.J., Garcia E.; Insights into the evolution of Yersinia pestis through whole-genome comparison with Yersinia pseudotuberculosis."; Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004). EMBL; BX936398; CAH19850.1; -; Genomic_DNA. G.; Go:0016029. C: membrane; IEA. InterPro; IPR000791; Grpl_Fun34_YaaH. Propon; P0010188; Grpl_Fun34_YaaH; 1.
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EMBL; AAER01000010; EAR07599.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP-dependent helicase activity; IEA.
GO; GO:0003676; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:Hydrolase activity; IEA.
GO; GO:0016787; F:Hydrolase activity; IEA.
InterPro; IPR01165; DEAD.
InterPro; IPR01165; DEAD.
InterPro; IPR01165; DEAD.
InterPro; IPR01165; DEAD.
INTERPRO; IPR01165; Helicase_C.
FEan; PF00270; Helicase_C.
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Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 851 AA; 98508 MW; 1891EC62ADCF9D28 CRC64;
                                                                                                                                                                                                                                                                                                       203 AA; 21644 MW; A21F2175B2ABCA0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
YDPA. Lin1/Skiz family RNA SFII helicase (Fragment)
ORFNames=cgd5_3870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.2%; Score 46; DB 2;
90.0%; Pred. No. 28;
tive 0; Mismatches 1
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2; Mismatches
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Pred. No.
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SMART; SM00490; HELICC; 1.
ATP-binding; Helicase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                   62.2%;
57.1%;
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Best Local Similarity 57....
Best Local Similarity 57....
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QSCQ75;
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546 MALKKINLHN 555
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 203 AA;
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Matches
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RESULT 16

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RESULT 20
QBEBD7 SHE
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RN UNCLECTIDE SEQUENCE.

RY WICKLECTIDE SEQUENCE.

RY ASSECT 12472 / DEM 30191;

RY WICKLECTIDE SEQUENCE.

RY VARGAGE 12472 / DEM 30191;

RY VARGAGE 2288280; PubMed=14560782; DOI=10.1073/pnas.1832124100;

REDINE=2288280; PubMed=14560782; DOI=10.1073/pnas.1832124100;

RA ANGENCE 124. R. Anderde F.C., de Almeida LG.P., de Anueida R.F.F.,

Antonio R.V., Almeida F.C., de Almeida LG.P., de Anueida R.F.F.,

RA Alve-Gomes J.A., Andrade E.M., Battaus L.A.M.

Antonio R.V., Almeida F.C., Berger G., Bogo M., Bonatto S.,

RA Actofit-Filho S., Azevedo V. Baptista A.J., Bataus L.A.M.

RA Alve-Somes J.A., Cardedo D.D.P., Carneiro N.P., Carraro D.M.,

Cardapon J.V. Cardedo D.D.P., Carneiro N.P., Carraro D.M.,

Cardanato A.M., Cardedo D.C., R., Freitas N.S.A., Ferraro D.M.,

Cartapadia D., Grisard E.C., Hanna E.S., Jardim S.N., Farro J.A.,

RA Andella R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Andella R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Andella R.T., Gomes E.A., Concalves P.R., Grangeiro T.B.,

RA Andella R.T., Marico G.P., Marahhao A.C., Jardim S.N., Laurino J.,

RA Andella R.M., Pinto L.S.R.C., Percetta J.G., Oliveira S.C.,

RA Anton S.M.Z., de Medeiros S.R.B., Meisener R.V., Moreira M.A.,

Anton D., Soarces C.M.A., Schneider M.P.C., 
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                                                                                                                                                                                                                                                                       Gaps
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaces, Chromobacterium.
WCBI_TaxID=536;
                                                                                                                                                                               Query Match 59.5%; Score 44; DB 2; Length 185; Best Local Similarity 50.0%; Pred. No. 14; Matches 7; Conservative 3; Mismatches 4; Indels
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Pfam; PF01184; Grp1_Fun34_YaaH; 1.
ProDom; PD01188; Grp1_Fun34_YaaH; 1.
Complete Proteome.
SEQUENCE 185 AA; 20227 MW; 65AF87115A3B0560 CRC64;
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01-MRA-2004 (TrEMBLrel. 26, Created)
01-MRA-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable membrane protein.
                                                                                                                                                                                                                                                                                                                                         1 MGYGMALSKINLHN 14
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15 MGFGMTTVLLNIHN 28
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Best Local Similarity 50.01
Matches 7; Conservative
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SEQUENCE 186 AA;
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RN WCLEDTIDE SEQUENCE.

RN WCLEDTIDE SEQUENCE.

RN Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., RA Read T.D., Eisen J.A., Seehadri R., Ward N.L., Merhe B.A., RA Read T.D., Eisen J.A., Sepaladri R., Ward N.E., Merhe E.A., Berry K.J., DeBoy R.T., Dodson R.J., Durkin A.S., RA Haff D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., RA Haff D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., RA Lee K., Berry K.J., Lee C., Madlhevan J.J., Weddman J.F., Impraim M., Lee K., Berry K.J., Lee C., Moller J., Khouri H.M., Gill J., RA Utterback T.R., McDonald L.A., Feldhlyum T.V., Smith H.O., RA Utterback T.C., Nealson K.H., Fraser C.M., Smith H.O., R. Wenter J.C., Nealson K.H., Fraser C.M., Smith H.O., R. Wenter J.C., Nealson K.H., Fraser C.M., Smith H.O., Butterbuoll oneidensis, #1 sismilatory metal ion-reducing bacterium RT GGO: GO:0016020; C:membrane; IEA.

DR GO: GO:0016020; C:membrane; IEA.

DR ROSITE; PSOILI4; GTPL Fun34 YaaH.

DR PROSITE; PSOILI4; GTPL Fun34 YaaH; 1.

DR PROSITE; PSOILI4; GTPL Fun34 YaaH; 1.
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STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella.
NCBL_TAXID=70863;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
WCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.5%; Score 44; DB 2; Length 189; 50.0%; Pred. No. 15; tive 3; Mismatches 4; Indels
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01-070-2003 (TrEMBLrel. 24, Last sequence update)
01-071-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein VP0620.
OrderedLocusNames=VP0620;
                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gprl/fun34/yamH family protein.
OrderedLocusNames=SO3588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI; 196 AA.
                    PRT; 189 AA.
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14 MGFGMTTILLNIHN 27
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Q87S04;
77 SHEON
QGEBD7 SHEON PRELIMINARY;
Q8EBD77;
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                                                                                                                                                                Shewanella oneidensis.
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SEQUENCE 189 AA;
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1 MGYGMALSKINLHN 14

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[1]
NUCLEOTIDE SEQUENCE.
                      SEQUENCE
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Best Local Similarity
                                       STRAIN=CMCP6
[1]
NUCLEOTIDE
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTION Campanaro S., D'Angelo M., Simonato F., Vitulo N.,

Leauro F.M., Cestaro A., Malacrida G., Simionati B., Cannata N.,

Romualdi C., Bartlett D.H., Valle G.;

"Life at depth: Photobacterium profundum genome sequence and expression analysis.";

Science 307:1459-1461[2005).

EMBL, CR378671; CAG20799-1; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IRA.

RILEPERO; IPRO00791; GTPL Fun34 YaaH.

ProDom; PD010188; GTPL Fun34 YaaH; 1.

PRODOM; PD010188; GTPL Fun34 YaaH; 1.

ROMPLEE PROSITE; PS01114; GRPL FUN34 YAAH; 1.

ROMPLEE DIOLOGN GENIL FUN34 YAAH; 1.

ROMPLEE DIOLOGN GENIL FUN34 YAAH; 1.
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Batceria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
NCBI TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative membrane protein.
Name=STY0009, OrderedLocusNames=PBPRA2415;
Phycobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria, Proteobacteria, Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 197;
Pred. No. 15;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                      Length 196;
                                                                                                                                                                                                                                                                                Indels
                 EMBL; BA00031; BAC5888.1; -; Genomic_DNA.
CO; GO:0016020; C:nembrane; IEA.
InterPro; IRR000791; Grp1 Fun34 YaaH.
ProDom; P0010184; Grp1 Fun34 YaaH; 1.
ProDom; P0010188; Grp1 Fun34 YaaH; 1.
PROSITE; PS01114; GPP1 Fun34 YaaH; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 196 AA; 20930 MW; 8FECFC8E367DDA11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                3; Mismatches
    from that of V. cholerae.";
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Predicted membrane protein.
OrderedLocusNames=VV10416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGYGMALSKINLHN 14
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14 MGFGMTTILLNIHN 27
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Best Local Similarity 50...
Ti Conservative
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QGLPH7 PHOPR PRELIMINARY;
QGLPH7;
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QBDF09;
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Best Local Similarity 50.0
Matches 7; Conservative
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MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Hoddelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Bragol I.,
Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
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Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.

VGBI_TaxID=666,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Length 197;
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                 "Complete genome sequence of Vibrio vulnificus CMCP6."; submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016798; AA008939.1; -; Genomic_DNA. GO; GO:0016020; c:membrane; IEA. InterPro; IPRE000791; Grpl Fun34 YaaH. FroDom; PF01184; Grpl Fun34 YaaH; 1. ProDom; PD010188; Grpl Fun34 YaaH; 1. Complete proteome. SEQUENCE 197 AA; 21066 WW; E1781C8FF21B08B9 CRC64;
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GO; GO:0016020; C:membrane; IEA.

GD: GO:0016020; C:membrane; IEA.

InterPro; IFR000791; Grpl_Fun34_YaaH.

ProDom; PD010188; Grpl_Fun34_YaaH; 1.

ProDom; PD010188; Grpl_Fun34_YaaH; 1.

Complete proceome; Hypothetical procein.

SEQUENCE 197 AA; 21120 MW; 5CD361817EB954E1 CRC64;
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Last annotation update)
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50.0%; Pred. No. 15;
tive 3; Mismatches
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EMBL; AE004162; AAF93935.1; -; Genomic_DNA.
PIR; F82282; F82282.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TEMBLEE]. 15,
01-0CT-2000 (TEMBLEE]. 15,
01-0M-2003 (TEMBLEE]. 24,
Hypothetical protein VC0770,
OrderedLocusNames=VC0770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.v...
Best Local Similarity 50.v...
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14 MGFGMTTILLNIHN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGYGMALSKINLHN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KTWO_VIBCH PRELIMINARY;
Q9KTWO;
                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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Gaps

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NUCLECTEDE SEQUENCE.

RE GALGAD JULIO SEQUENCE.

RE GALGAD JULIO SEQUENCE.

RE GALGAD JULIO SEQUENCE.

RA GALGAD JULIO SEQUENCE.

RA GALGAD JULIO SEQUENCE.

RA FILTHUR W., CALVO S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Smith K.,

RA Jinton L., McEwan P., White O., White R.H., de Macario E.C.,

RA Ferry J.A., Liw J., White O., White R.H., de Macario E.C.,

RA Ferry J.A., Jiw M., Liw J., White O., White R.H., de Macario E.C.,

RA Ferry J.C., Jarrell K.P., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

ROG GO:0016020; C:membrane; IEA.

DR RMB; AR011113; AAMO7358.1; .; Genomic_DNA.

DR FADD, PRO1018; Grpl_Fun34_YaaH; 1.

DR PROSITE; PRO1114; GRPl_Fun34_YaaH; 1.

REMB; PROSITE; PRO1114; GRPl_Fun34_YaAH; 1.

REMB; PROSITE; PRO11184; APAN 21734 MW; BF6013C034C0DAFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Transcriptional regulator.
Transcriptional regulator.
Xanthomonas campestris pv. campestris str. 8004.
Bacteria, Fortecbacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomona, Pactobacteria, Gammaproteobacteria, Xanthomonadales,
NGEL TaxID=314565,
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Archaea, Buryarchaeota, Methanomicrobia, Methanosarcinales,
Methanosarcinacae, Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2; Length 201;
Pred. No. 16;
3; Mismatches 4; Indels
     Score 44; DB 2; Length 200;
Pred. No. 16;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Fun34 related protein.
OrderedLocusNames=MA4008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AA.
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           59.5%;
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                                                                                                                                                                                                                                                                                                      29 MGFGMTTVLLNIHN 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBTIY1 METAC PRELIMINARY;
QBTIY1;
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Best Local Similarity 50.0.
Best T; Conservative
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Q4UYJO XANCP PRELIMINARY;
Query Match
Best Local Similarity 50.0°
Matches 7; Conservative
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NUCLEOTIDE SEQUENCE
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08 TIYL MET
10 08 TIYL
DT 01-JU
DT 01-JU
DT 01-JU
DE FUN34
CON Metha
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RY NUCLEOTIDE SEQUENCE.

RY MUCLEOTIDE SEQUENCE.

RY MEDLINE=2120827; PubMed=12125824;

REDLINE=2120827; PubMed=12125824;

ROBDLINE=2120827; PubMed=12125824;

RY MATINE=2120827; PubMed=12125824;

RY Hospenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

RA Mattinez-Arias R., Henne A., Wiezer A., Bacumer S., Jacobi C.,

RY Hospenmann H., Lienard T., Christmann A., Boemeckel M., Steckel S.,

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,

RH The genome of Methanosarcina mazei: evidence for lateral gene

RY The genome of Methanosarcina mazei: evidence for lateral gene

RY The genome of Methanosarcina and Archaea."; Goologo.

RY Microbol. Biotechnol. 4:453-461(2002).

RY REML, AR01316; AAM30599.1; Genomic_DNA.

DR RYBL, AR01316; AAM30599.1; Genomic_DNA.

DR FRAM, PFOLNS4; Grpl Fun34 YaaH; 1.

DR FROM: PDOLUBS; Grpl Fun34 YaaH; 1.

RY PROSITE; PROLI114; GFRl-FUN34 YaAH; 1.

KW Complete proteome.

SEQUENCE 200 AA; 21621 MW; GFRAB042D9B70FF0 CRC64;
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BY NUCLECATIDE SEQUENCE.

WA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,

A Liao T.-L., Liu Y.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,

A Liao T.-L., Liu Y.-M., Chan H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

A Liao T.-L., Liu Y.-M., Chan H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

A Liao T.-L., Liu Y.-M., Chan H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

A Change C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;

The Comparative genome analysis of Vibrio vulnificus, a marine

RT "Comparative genome analysis of Vibrio vulnificus, a marine

RT Genome Res. 13.2577-2587(2001)

REMBL, BA00037; BAC33542.I.; Genomic_DNA.

BR MCO, GO.0016020; C:membrane; IEA.

BR RCO, GO.0016020; C:membrane; IEA.

BR REAM; PF01184; Grp1 Fun34 YaaH; 1.

PRODOM; P001108; Grp1 Fun34 YaaH; 1.

BR PRODOM; P001114; GPR1_FUN34_YAAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
07-UNN-2003 (TrEMBLrel. 24, Last annotation update)
07-CreatocusNamaes=MN0903;
Mchanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinacae; Methanosarcina.
[11]
                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=VVO778;
Vibrio vulnificus (strain YJO16).
Vibrio vulnificus (strain YJO16).
Vibrionaceae, Vibrio.
Vibrionaceae, Vibrio.
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                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Predicted membrane protein.
                                                                         197 AA
                                                                         PRT,
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14 MGFGMTTILLNIHN 27
                                                                   Q7MND9 VIBVY PRELIMINARY;
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OBPYF9_METMA
AC OBPYF9_A
AC OBPYF9_A
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DT 01-OCT-20
DT 01-UN-20
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STRAIN-ATCC 33913 / NCPPB 528;

MEDINE-22022145; PubMed=12024217; DOI=10.1038/417459a;

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A lameida N.F. Jr., Alves L.M.C., do Amaral A.M., Bercolnin M.C.,

A changed L.B.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,

Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

A ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

B El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Cardin B.C., Machado M.A., Madelra A.M., Machado M.A., Madelra A.M., Marchinez-Rossi N.M.,

Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins E.C., Meddanis J., Sena J.A.D., Silva C., de Souza R.F.,

A pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.T.D.,

Trindade dos Santoso M., Truffi D., Tsai S.M., White F.F.,

Romparison of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes of two Xanthomonas pathogens with differing the process of the genomes o
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                         Odan W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F., Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L., Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G., Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000843; HTH LacI.
InterPro; IPR001761; PerIplaBP/LacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae; Xanthomonas.
YCBI_TaxID=340;
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                                                                                                                                                                                                                                                                                                                                     Query Match 59.5%; Score 44; DB 2; Length 343; Best Local Similarity 66.7%; Pred. No. 27; Matches 8; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                    Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000050; AAY47883.1; -; Genomic DNA.
SEQUENCE 343 AA; 36846 MW; A30A81FB7DC8C057 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-2002 (TrEMBLrel. 22, Created)
1-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transcriptional regulator.
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EMBL; AE012454; AAM42626.1; -; Genomic_DNA.
HSSP; P03023; ICJG.
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Pfam; PF00532; Peripla BP 1; 1.
SMART; SM00354; HTH LACI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 GYSMLLSKLNRH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GYGMALSKINLH 13
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       STRAIN=8004;
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08P515_XANCP
08P515_XAC
AC 08P515_XAC
DT 01-0CT-20
DT 01-0CT-20
DT 01-0CT-20
DE Transcrip
GN Xanthomomo
OC Bacteria OC
C Bacteria OC
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Gaps

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3; Indels

Best Local Similarity Matches 8; Conserv

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STRAIN-PG1;
Pubmed=14762060; DOI=10.1101/gr.1673304;
Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J.,
Westberg J., Petrersson B., Uhlen M.;
The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
strain PG1T, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 14:221-227(2004).
EMBL, BX842644; CAE77306.1; -; Genomic DNA.
GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larimer F., Land M.; "Annotation of Deinococcus geothermalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geothermalis
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Deinococcus geothermalis DSM 11300.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSM 11300.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
probable nicotinic phosphoribosyltransferase (EC 2.4.2.11).
Name-pncB; OrderedLocusNames=MSC 0687;
Mycoplasma mycoides (subsp. mycoldes SC).
Bacteria; Firmcutes; Mollicutes; Mycoplasma.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Similar to merapendent hydrolase with the TIM-barrel fold.
ORFNames=DgeoDRAFT 0101;
Deinococcus geothermalis DSM 11300.
Bacteria; Deinococcus-Thermus; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.5%; Score 44; DB 2; Length 362; 66.7%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 AA; 41160 MW; 8121BF091281DFB9 CRC64;
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STRAIN=DSM 11300;
US DOE Joint Genome Institute (JGI-ORNL);
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                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Q4H6L8;
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                                                                     108 GYSMLLSKLNRH 119
                                                                                                                                                                                                                                                                       QEMST2 MYCMS PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GYGMALSKINLH 13
13
GYGMALSKINLH
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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Last sequence update)
Last annotation update)

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"The genome sequence of Clostridium tetani, the causative agent of tetanua disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

EMBL; AE015936; AA034739.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR005372; UPF0182;
Ffam; PF03699; UPF0182; 1.
Complete protecome:
EQUENCE 887 AA; 103741 MW; A92998D2EA3CB7D7 CRC64;
                                                                                                                                                                                     STRAIN-Massachusetts / E88;
MEDLINE-2245/253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                 Clostridium tetani.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae;
Clostridium.
      01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Conserved membrane protein. OrderedLocusNames=CTC00086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 70.0
les 7; Conservative
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417 GYGVAMSKVN 426
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                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                   NCBI_TaxID=1513;
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ID RS24 AERPE
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                                                                                                                                       Gaps
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Tetradon nigrovitidis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which is
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Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DD5J databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DD5J whole genome shotgun (WGS) entry whic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.5%; Score 44; DB 2; Length 694; 72.7%; Pred. No. 54; cive 3; Mismatches 0; Indels
                                                                                                Match 59.5%; Score 44; DB 2; Length 501; Local Similarity 53.8%; Pred. No. 39; 2; Indele 69 7; Conservative 4; Mismatches 2; Indele
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694 AA; 77492 MW; FDBB74F7D7F17FE7 CRC64;
                                                                  501 AA; 53099 MW; 13CFBB50B9CC64AB CRC64;
                                                                                                                                                                                                                                                                                                                                   CALLEAN TRANSLIED. 31, Created)
13-SEP-2005 (TEXMELTEL) 31, Last sequence update)
13-SEP-2005 (TEXMELTEL) 31, Last annotation update)
Chromosome 3 SCAF14975, whole genome shotgun sequence.
preliminary data.
EMBL, AAHE01000013; EAL81904.1; -; Genomic_DNA.
Hydrolase.
SEQUENCE 501 AA; 53099 MW: 13CFFFRRGEOGCCCAND
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; CAAE01014975; CAG06520.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                      694 AA
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                              (Fragment).
ORFNames=GSTENG00026906001;
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Best Local Similarity 72.,
Local Similarity 72.,
Local Similarity 72.,
12.,
14.
                                                                                                                                                                             1 MGYGMALSKINLH 13
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72 VAYGFSLSQLNLH 84
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                                                                                                    Query Match
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Gaps

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59.5%; Score 44; DB 2; Length 887; 70.0%; Pred. No. 68; 1. Mismatches 0; Indels

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=S9310319, PubMed=10382964
MEDLINE=S9310319, PubMed=10382964
MEDLINE=S9310319, PubMed=10382964
MEDLINE=S9310319, PubMed=10382964
MEDLINE=S9310319, PubMed=10382964
MINITY: Ankai A., Haikawa H., Yamazaki S., Haikawa Y.,
Jinno K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi I
Hosoyama A., Fukui S., Punahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
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                                                                                        30-May-2000 (Rel. 39, Created)
30-May-2000 (Rel. 39, Last sequence update)
10-May-2005 (Rel. 47, Last annotation update)
30S ribosomal protein 524e.
Name=rps24e; OrderedLocusNames=APE1132;
102 AA.
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InterPro; IPR01976; Ribosomal_S24E.
PANTHER; PTHR10496; Ribosomal_S24E; 1.
Pfant, PP01282; Ribosomal_S24e; 1.
     STANDARD;
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887 AA.

RESULT 33
089972 CLOTE PRELIMINARY; PRT;
1D Q89972 CLOTE TELIMINARY; PRT;
AC Q89972 DT 01-JUN-2003 (TYEMBLY 1.24, Created)

496 GISLSKISLHN 506

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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

NCBI_TaxID=229533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larimer F., Land M.; "Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anaeromyxobacter dehalogenans 2CP-C.
Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Myxococcaceae, Anaeromyxobacter.
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                                                                                                                                                DB 1; Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                         Indels
      ProDom, PD006052; Ribosomal_S24E; 1.
PROSTIE; PS00529; RIBOSOMAL_S24E; 1.
Complete proteome, Ribonucleoprotein; Ribosomal protein.
SEQUENCE 102 AA; 11858 MW; DEAA205AAFBD8066 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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4CE 214 AA; 22798 MW; 9C3059FF2E547170 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA.
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3; Mismatches
                                                                                                                                                                                                         2; Mismatches
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US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.1%; Score 43; Best Local Similarity 50.0%; Pred. No. 3 Matches 7; Conservative 3; Mismatch
                                                                                                                                                      Score 43;
                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=FG02118.1;
                                                                                                                                                   58.1%;
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
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Q4IKZO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4NQB2_9DELT PRELIMINARY;
Q4NQB2;
                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                   2 GYGMALSKINLH 13
                                                                                                                                                                                                                                                                                                                         60 GYGAGLSKVRVH 71
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ORFNames=AdehDRAFT_0850;
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                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=290397;
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
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Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA, Burkhaller B., Nusbaum C., Abouelleil A., Bloom T., Boguslavkiy L.,
RA, Boukhgalter B., Butler J., Calvos S.E., Camarata J., Chang J.,
Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA, Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA, Gardyna S., Gnerre S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA, Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA, Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA, Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA, Mathews C., MacCean C., MacGonald P., Major J., Manning J.,
RA, Mithowa T., Mangay V., Murphy T., Naylor J., Manning J.,
RA, Michar T., Manga W., Murphy T., Naylor J., Mayor B.,
RA, Rachupka A., Ramasamy U., Raymond C., Nounell P., O'Neil D.,
RA, Schupback R., Seamen S., Severy P., Smirnov S.,
RA, Talamas J., Tesfaye S., Theodore J., Topham K., Texvers M.,
RA, Wassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA, Lander E., Stange-Thomann V., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Rander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Lander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Rander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Rander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Rander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
RA, Rander E., Stange-Thoman J., Zembek L., Zimmer A., Zody M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE [LARGE SCALE MENA].
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P.,
Eaton D., Foster J.S., Grimaidal C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Name-SLITRK1; Synonyms-KIAA1910, LRCC12; ORFNames-UNQ233/PRO266; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Fusarium graminearum genome sequence.";
Submittend (FEB=2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 97;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 541 AA; 60552 MW; D9EBFE69CD5AFDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
EMBL; AACM01000111; EAA69749.1; -; Genomic_DNA.
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05-JUL-2004 (Rel. 44, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 AA.
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153 LGYGLLLSEGNVH 165
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NA Res. 8:179-187(2001).
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es 7; Conservative
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Potential. SLIT and NTRK-like protein

Repeat;

Leucine-rich repeat;

SIGNAL

Potential.

LERR 1. LERR 2. LERR 3. LERR 5. LERR 6. LERR 7. LERR 9. LERR 9. LERR 10. LERR 11. LERR 11.

REPEAT REPEAT REPEAT REPEAT

REPEAT REPEAT

18 57 81 81 1105 1130 1153 1178 1178 374

CHAIN TRANSMEM REPEAT REPEAT REPEAT

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WUCLECTIBE SEQUENCE (LARGE SCALE GENOWIC DIA):

A DUNHAM A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,

A Anscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

A Anscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

Ashwell R.I.S., Babbage A.K., Bagguley C.L., Balley J., Bannerjee R.,

Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,

Chapman J.C., Clamp M.B., Clark S.Y., Clarke G., Clee C.M.,

Chapman J.C., Clamp M.B., Clark S.Y., Clarke G., Clee C.M.,

Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

Deloukas P., Dhami P., Dunham I., Dunn M. Earthroul M.E.,

Rilington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

A anner P. Garnett J., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,

Ring A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,

Rashreghi-Mohammadi M., Mclaren S.J., McMurray A., Milne S.,

Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,

Rallming L., Wray P.W., West A.P., Whitehead S.L., Willey D.L.,

Williming L., Waray P.W., Wright M.W., Young L., Coulson A., Durbin R.,

All M., Malleton J.E., Back S., Bentley D.R., Rogers J., Ross M.T.;

Rallming L., Waray P.W., Wright M.W., Young L., Coulson A., Durbin R.,

All M., DNA sequence and analysis of human chromsome 13.";

Alture 428:522-528(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE BRAIN, and Brain tumor; Property of the property of the
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yandlen R.L., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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Gaps

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Score 42; DB 1; Length 696; Pred. No. 1.2e+02; 4; Mismatches 0; Indels

Local Similarity 63.6 les 7; Conservative

Query Match

Matches

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|::|||::||| 493 GVSLSKLSLHN 503 4 GMALSKINLHN 14

E0E9ACEDE0F0ACEC CRC64;

77735 MW; 56.8%;

696 AA;

REPEAT REPEAT REPEAT REPEAT SEQUENCE

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NUCLECIDES SEQUENCE LURANS SCALES FRANCE IN TRANSPINCE TO STATE TO
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelia, Butentia, Butheria, Butarchontoglires, Glires, Rodentia, Sciurognathi, Murcidae, Muridae, Murinae, Mus.
(NCB_TAXID=10090)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAGE.

PubMed=14550773; DOI=10.1016/S1044-7431(03)00129-5;

Aruga J., Mikoshiba K.;
"Identification and characterization of Slitrk, a novel neur transmembrane protein family controlling neurite outgrowth."
Mol. Cell. Neurosci. 24:117-129(2003).
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                                 SLIKI MOUSE STANDARD; PRT; 696 AA. 081KI MOUSE (0810C1); 09CKLD; 09CKLD; 05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) SLIT and NTRK-like procein 1 precursor. Musme-Slitkl; Synonyms-Slikl; Mus musculus (Mouse).
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EMBL, AB067497; BAB67803.1; ALT_INIT; mRNA. EMBL; AV358289; AAQ88656.1; -; mRNA. BMBL, AL355481; CAC37488.1; -; Genomic_DNA. Ensembl; ENSG00000178325; Homo saplens. HGNC; HGNC; 20297; SLITEKI.

HGNC; HGNC: 20297; SILTRKI.
INTERPO; IPRO01611; ILRR.
INTERPO; IPRO01683; ILRR.
INTERPO; IPRO01983; ILRR.
PFam; PF00560; ILRR 1; 8.
SMART; SM00369; ILRR. TYP; II.
SMART; SM00082; ILRR. TYP; II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazuwa N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney B., Hayashizaki Y.; Maraki Y., Itoh M., Coshina and C., Chipata K., Chilagawa A., Oshinasa K., Maraki Y., Cander E.S., Rogers J., Birney B., Hayashizaki Y.; Maraki Y., Chill-length cDNAs."; Analysis of the mouse transcriptome based on functional annotation of Go,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                  -: FUNCTION: Enhances neurite outgrowth.
-: SUBCELLUIAR LOCATION: Membrane-bound (Potential).
-: SUBCELLUIAR LOCATION: Membrane-bound (Potential).
-: TISSUE SPECIFICITY: In the adult, significant expression is detected only in the brain. Broadly expressed in embryonic brain with highest expression in subventricular zone, subplate, cortical plate, pyramidal cell layer of hippocampus, thalamus and hypothalamus where levels are highest in ventromedial hypothalamus and medial part of periacqueductal gray matter. Also expressed in mantle layer of spinal cord and in lateral and medial motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: In the embryo, expressed from day 10-12 and continues through later gestational development and into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 696;
Pred. No. 1.2e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the SLITRK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B3F23AF1A28B9E1B CRC64;
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EMBL; AK014285; BAB29244.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI; MGI:2679446; Slitzkl.
MGI; MGI:2679446; Slitzkl.
GO; GO:0007409; P:axonogenesis; IDA.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR000372; LRR_Vterm.
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SMART; SMOD369; LRR TYP; 2.
SMART; SMOD082; LRRCT; 2.
SMART; SMOD013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leucine-rich repeat; Repeat; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.8%;
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Best Local Similarity 63.00
T; Conservative
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470
495
696 AA;
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MEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Riausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Romstein M.J., Webwan P.J., McKernan K.J., Mallany S.J.,
Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Rothicing A., Schmutz J., Mysers R.M.,
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Rothertield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. W. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
M. Genneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Pred. No. 1.2e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC051738, AAH51738.1; -; mRNA.
InterPro; IPR001611; LRR.
InterPro; IPR00363; LRR. Cterm.
InterPro; IPR003591; LRR. typ.
Pfam; PF00560; LRR. 1; 8.
PRINTS; PR0019; LEURICHRPT.
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SEOUENCE 696 AA: 77721 MW; FC82AFCCD2E0ADBD CRC64;
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GSRAC4;
G1-FBB-2005 (TrEMBLrel. 29, Created)
01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459G0529.
                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Slit and trk like 1 protein.
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SMART; SM00082; LRRCT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.8%;
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QSUSI6_HUMAN PRELIMINARY;
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 GVSLSKLSLHN
                                                                                                                                                                                                                                  Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
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QSRAC4 PONPY
ID QSRAC4_PO
AC QSRAC4,DT 01-FEB-2
DT 01-FEB-2
DT 01-FEB-2
DT 01-FEB-2
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Gaps

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GN Name=DKFZP459G0529;

OS PROMGO PYGRAGUEN (Coranjutan).

OC Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OX NCBI TaxID=9600;

RN [1]

RN [1]

RN NUCLECTIDE SEQUENCE.

RG THE German CDNA Consortium;

RA Denager A., Fobo G., Han M., Wiemann S.;

RG The German CDNA CONSORTIUM;

RA OBANGER IN., Boecher M., Wiemann S.;

RI SUMMITTED SEQUENCE.

RI SUMMITTED SEQUENCE.

RE MEL; CR859094; CAH91286.1; -; mRNA.

DR INTERPO: IPRO01431; LRR.

Pfam, PFO0560; LRR.1; 9.

DR RINTS; PRO0191; LEURICHRPT.

DR SMART; SW000369; LERR IYP.

SGOUENCE 696 AA; 77699 WW; 7AF48D3844D97CBC CRC64;

QUESTY MATCH

BOST MATCH SW00369; LRR.

GOUST MATCH SW00369; LRR.

DR SMART; SW00369; LRR.

SGOUENCE 696 AA; 77699 WW; 7AF48D3844D97CBC CRC64;

GOUST MATCH SW00369; LR.

BEST Local Similarity 63.6%; Pered. No. 1.26+02;

BEST Local Similarity 63.6%; Pered. No. 1.26+02;

BEST Local Similarity 63.6%; Pered. O, Indels 0; Gaps 0;
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Search completed: May 13, 2006, 08:13:59 Job time : 232 sec8

4 GMALSKINLHN 14 |::|||::||| 493 GVSLSKLSLHN 503

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